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Research Article

Taxonomy and phylogeny of Irpicaceae and Meruliaceae (Polyporales, Basidiomycota) with descriptions of four new species from southwestern China

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Abstract

Wood-decaying fungi play crucial roles as decomposers in forest ecosystems. In this study, four new wood-inhabiting fungi from Yunnan Province of southwest China—*Crystallicutis albomarginata*, *Efibula glossophora*, *E. punctata*, and *Scopuloides farinacea*—are described and illustrated based on morphological and molecular evidence. The species *C. albomarginata* is characterized by its slightly pink to orange basidiomata when dry, a monomitic hyphal system with simple septa, and narrowly ellipsoid basidiospores measuring 3.7–4.4 × 1.9–2.8 µm. The taxon *E. glossophora* is characterized by its hard, membranous, slightly yellow to yellow basidiomata; a monomitic hyphal system with simple-septate generative hyphae; and ellipsoid basidiospores measuring 3.8–6 × 2.6–3.7 µm. The species *E. punctata* is characterized by its membranaceous, slightly gray to pale brown basidiomata; a monomitic hyphal system with simple-septate generative hyphae; and ellipsoid basidiospores measuring 4.3–6.2 × 2.2–3.3 µm. Additionally, the taxon *S. farinacea* is characterized by its coriaceous, pale cream to buff basidiomata; a monomitic hyphal system with simple-septate generative hyphae; and ellipsoid basidiospores measuring 2.8–3.5 × 1.4–2 µm. Sequences of the internal transcribed spacer region (ITS), the large subunit nuclear ribosomal RNA gene (nLSU), the translation elongation factor 1-α gene (TEF1), the largest subunit of RNA polymerase II (RPB1), and the second subunit of RNA polymerase II (RPB2) of the studied samples were employed, and phylogenetic analyses were performed using maximum likelihood, maximum parsimony, and Bayesian inference methods, ensuring the robustness of the findings. Based on the combined ITS + nLSU + RPB1 + RPB2 + TEF1 dataset, phylogenies of the two families Irpicaceae and Meruliaceae were constructed. In these analyses, *Crystallicutis albomarginata* was recovered as sister to *C. serpens*; *E. punctata* as sister to *E. intertexta*; *Efibula glossophora* as closely related to *E. intertexta* and *E. hainanensis*; and the new species *S. farinacea* as sister to *S. allantoidea*.

Key words: Four new species, molecular systematics, taxonomy, wood-inhabiting fungi, Yunnan Province

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Introduction

Fungi play vital roles in forest ecosystems as endophytes, pathogens, and saprobes (Wei and Dai 2004; Dai 2012; Cui et al. 2019; Bhunjun et al. 2022; Dong et al. 2024; Hyde et al. 2024; Yang et al. 2025a). The number of species in the kingdom Fungi is estimated to range from 2.2 to 13.2 million, with the latest estimate suggesting 2 to 3 million species. However, only around 150,000 species have been named and classified to date (Dai and Zhuang 2010; Bhunjun et al. 2022; He et al. 2024; Hyde et al. 2024; Zhao et al. 2024). Undescribed fungi therefore represent a vast potential resource at a time when there is an urgent need to discover new sources of food, antibiotics, and metabolites with biotechnological, industrial, and pharmaceutical applications (Hyde et al. 2019).

Species in the phlebioid clade of the Polyporales are wood-inhabiting fungi associated with white rot and typically produce crust-like or corticioid basidiomata with smooth or variously shaped hymenophores (Chen et al. 2021; Li et al. 2025). Within this clade, three well-supported subclades are recognized: the families Phanerochaetaceae Jülich, Irpicaceae Spirin & Zmitr., and Meruliaceae Rea. The ecology, species diversity, taxonomy, and molecular systematics of taxa in these families have been extensively studied (Floudas and Hibbett 2015; Miettinen et al. 2016; Justo et al. 2017; Zmitrovich 2018; Chen et al. 2021; Li et al. 2022, 2023; Lira et al. 2022; Motato-Vásquez et al. 2022; Wang et al. 2023; Yuan et al. 2023; Zhao et al. 2023; Xu et al. 2024; Li et al. 2025; Liu et al. 2025a).

In terms of morphology, the Irpicaceae comprises corticioid species or resupinate to pileate polypores. The hyphal system is usually monomitic, rarely dimitic; generative hyphae are typically simple-septate, rarely nodose-septate. Cystidia are often absent, and basidiospores are generally thin-walled, smooth, and colorless. The Meruliaceae includes corticioid species, resupinate or pileate polypores, or pileate hydnaceous species, which are often ceraceous in appearance. The hyphal system is usually monomitic, rarely dimitic, and tightly arranged; generative hyphae are usually nodose-septate, rarely simple-septate. Cystidia are often present, and basidiospores are typically thin-walled, smooth, and colorless (Justo et al. 2017; Chen et al. 2021; Li et al. 2025).

The genus *Efibula* Sheng H. Wu was introduced by Wu (1990) and typified by *E. tropica* Sheng H. Wu. This genus is characterized by membranaceous, subceraceous to ceraceous, buff-brownish basidiomata with smooth-tuberculate hymenophore, a subiculum of dense texture, a monomitic hyphal system with typically simple-septate hyphae, and an absence of cystidia. Cystidioles and hyphidia are present in some species (Chen et al. 2021). Species in *Efibula* are morphologically similar and can be distinguished only by slight variations in basidiospore size and shape, the presence of cystidioles and hyphidia, and hymenial configuration and color (Chen et al. 2021). Based on the MycoBank database (http://www.mycobank.org, accessed on 25 April 2025) and Index Fungorum (http://www.indexfungorum.org, accessed on 25 April 2025), the genus *Efibula* has registered 29 specific and infraspecific names, with 26 species widely recognized (Hyde et al. 2024).

Currently, DNA sequence-based classification and identification have become the standard in fungal taxonomy. Revisiting the taxonomy of *Phanerochaete* P. Karst. using a four-gene dataset revealed that four *Efibula* species clustered together and grouped with *Byssomerulius corium* (Pers.) Parmasto (Floudas and

Hibbett 2015). A phylogenetic study revising the family-level classification of the Polyporales showed that *E. clarkiae* Floudas & Hibbett and *E. gracilis* Floudas & Hibbett grouped together, with *Efibula* species nested within Irpicaceae (Justo et al. 2017). Chen et al. (2021) demonstrated through multigene phylogenetic analyses that *Efibula* was paraphyletic in the phylogenetic tree, although there was insufficient morphological evidence to support the recognition of separate genera. Dong et al. (2024) introduced a new *Efibula* species, characterized morphologically and analyzed phylogenetically using ITS, nLSU, and TEF1 sequences.

The genus *Crystallicutis* El-Gharabawy, Leal-Dutra & G.W. Griff. was typified by *Crystallicutis damiettensis* El-Gharabawy, Leal Dutra & G.W. Griff. (El-Gharabawy et al. 2021). *Crystallicutis* differs from other Irpicaceae members by its encrusted subicular hyphae and typically yellow hymenial surface when fresh. Basidiomata are resupinate with smooth, tuberculate, papillate, merulioid, or occasionally poroid hymenophores, usually honey-yellow (but occasionally rosy, reddish, or greenish), waxy, with white margins. Subicular hyphae, and sometimes the hymenium/subhymenium, are encrusted with crystals associated with darker resinous granules. The hyphal system is monomitic, usually with clamp connections. Basidia are cylindric-clavate; basidiospores are hyaline, smooth, ellipsoid, non-amyloid, and non-dextrinoid (El-Gharabawy et al. 2021). Based on MycoBank and Index Fungorum (accessed on 25 April 2025), the genus *Crystallicutis* has registered four specific and infraspecific names, with four species widely recognized (Hyde et al. 2024).

The taxonomy of Polyporales is complicated by the variability of key morphological characters across families and genera but is gradually being resolved through molecular phylogenetic analyses (El-Gharabawy et al. 2021). Multigene phylogenetic analyses based on ITS, LSU, TEF1, RPB1, and RPB2 loci placed *Crystallicutis damiettensis* in Irpicaceae and formed a distinct clade with *Ceraceomyces serpens* (Tode) Ginns and several other previously unnamed taxa, thus establishing the new genus *Crystallicutis* (El-Gharabawy et al. 2021).

Meruliaceae was introduced by Rea in 1922 and has been strongly supported as a monophyletic clade in Polyporales. To date, 28 genera have been described in Meruliaceae (Floudas and Hibbett 2015; Justo et al. 2017; Chen et al. 2021; Li et al. 2025). *Scopuloides* (Massee) Höhn. & Litsch. forms a well-supported monophyletic group (Li et al. 2025). The genus *Scopuloides*, typified by *S. hydnoides* (Cooke & Massee) Hjortstam & Ryvarden, has been recovered as monophyletic within Meruliaceae and includes species from Asia, Europe, North America, and the Neotropics (Chen et al. 2021). *Scopuloides* species are typically ceraceous, with white to buff basidiomata, and odontioid, hydnoid, or grandinioid hymenophores. The genus is characterized by a compact subiculum with agglutinated, short-celled subicular hyphae, short basidia, small basidiospores, and the presence of lamprocystidia (Wu 1990; Gilbertson and Nakasone 2003; Bernicchia and Gorjón 2010). Based on MycoBank and Index Fungorum (accessed on 25 April 2025), *Scopuloides* has registered 15 specific and infraspecific names, with 10 species widely recognized (Hyde et al. 2024).

Species diversity, taxonomy, and multigene phylogeny of the phlebioid clade (Phanerochaetaceae, Irpicaceae, Meruliaceae) of Polyporales Gäum. have shown that four species of *Scopuloides* grouped together based on nuc rDNA ITS1-5.8S-ITS2, 28S rDNA, RNA polymerase II largest subunit (RPB1), RNA polymerase II second largest subunit (RPB2), and translation elongation factor 1-α

(TEF1), with all species clustering within Meruliaceae (Chen et al. 2021). Multigene phylogeny and taxonomy of the wood-inhabiting fungal genus *Phlebia* sensu lato Fr. (Polyporales, Basidiomycota) indicated that four *Scopuloides* taxa were nested within Meruliaceae and closely related to *Climacodon* P. Karst. and *Luteochaete* C.C. Chen & Sheng H. Wu, based on ITS+nLSU+TEF1+mtSSU+GAPDH+RPB1+RPB2 sequences (Zhao et al. 2023). Phylogenetic analyses were carried out on two datasets—ITS+nLSU and five-gene (ITS+nLSU+RPB1+RPB2+TEF1) sequences—to further explore species diversity in Meruliaceae, clarify the validity and circumscription of select genera, and contribute to a well-supported and robust phylogeny of the family (Li et al. 2025).

During investigations of wood-inhabiting fungi in Yunnan Province, China, four undescribed species were discovered and are introduced herein. The aims of this study are to confirm the taxonomic affinities of the new species and to carry out a phylogenetic and taxonomic study based on ITS, nLSU, RPB1, RPB2, and TEF1 sequences to elucidate the relationships among representative species of Irpicaceae and Meruliaceae. Accordingly, four new species—*Crystallicutis albomarginata*, *Efibula glossophora*, *E. punctata*, and *Scopuloides farinacea*—are proposed, with descriptions and illustrations based on morphological characteristics and phylogenetic analyses.

Materials and methods

Sample collection and fungarium specimen preparation

Basidiomata were collected from Yunnan Province, China. Fresh specimens were photographed in situ using a Nikon D7100 digital camera, and macroscopic features were recorded in the field. All photographs were focus-stacked using Helicon Focus software. Specimens were then transported to a field station and dried using an electric food dryer at 45 °C. Once fully dried, the samples were sealed in envelopes and zip-lock plastic bags, labeled, and deposited in the fungarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos taken *in situ* and in the laboratory. The macro-morphology was based on both fresh and dried specimens. The color terms used in the descriptions followed Anonymous and Petersen (Anonymous 1969; Petersen 1996). Micromorphological data were obtained from the dried specimens and observed under a light microscope following previous studies (Dai 2010; Wu et al. 2022a). Sections were mounted in 5% KOH and 2% phloxine B dye ($C_{20}H_2Br_4Cl_4Na_2O_5$), and other reagents, including cotton blue and Melzer's reagent, were also used to observe micromorphology following Wu et al. (2022a). To show variation in spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. At least thirty basidiospores from each specimen were measured. Stalks were excluded from basidia measurements, and the hilar appendage was excluded from basidiospore measurements. The following abbreviations were used: CB = cotton blue, CB– = acyanophilous, KOH = 5%

potassium hydroxide, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid. W = mean spore width (arithmetic average for all spores), L = mean spore length (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, and n (a/b) = number of spores (a) measured from a given number (b) of specimens (Guan and Zhao 2021; Wu et al. 2022a; Wang et al. 2023).

Molecular phylogeny

Genomic DNA was extracted from dried basidiomata using a cetyltrimethylammonium bromide rapid plant genome extraction kit (Aidlab Biotechnologies Co., Ltd., Beijing) according to the manufacturer's instructions: a small piece of dried fungal specimen (about 30 mg) was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 mL centrifuge tube, suspended in 0.4 mL of lysis buffer, and incubated at 65 °C in a water bath for 60 min. After that, 0.4 mL of phenol-chloroform (24:1) was added to each tube, and the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 mL of supernatant was transferred to a new tube and mixed with 0.45 mL of binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 mL of inhibitor removal fluid was added to the AC for centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 mL of washing buffer, the AC was transferred to a clean centrifuge tube, and 100 µL of elution buffer was added to the middle of the adsorbed film to elute the genomic DNA (Zhao et al. 2012). The primer pair ITS5 and ITS4 (White et al. 1990) was used to amplify the ITS region. The primer pair LR0R and LR7 (Vilgalys and Hester 1990; Rehner and Samuels 1994; Yang et al. 2025b) was used to amplify the nuclear LSU region. The RPB1 region was initially amplified with RPB1-Af and RPB1-Cf (Matheny et al. 2002). RPB2 was amplified with the primer pair bRPB2-6F and bRPB2-7.1R (Liu et al. 1999; Matheny et al. 2002; Matheny 2005). TEF1 was amplified with the primer pair EF1-983F and EF1-2218R (Dong et al. 2024). PCR was performed following Dong et al. (2024). All newly generated sequences were deposited in the GenBank database. All sequences are listed in Table 1.

The sequences were aligned initially by using MAFFT (https://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy and then manually optimized in BioEdit and Aliview version 1.27 (Hall 1999; Yang et al. 2025b). The dataset is aligned first, and then ITS, nLSU, RPB1, RPB2, and TEF1 sequences are combined with Mesquite version 3.51. To determine the phylogeny, we compiled an ITS+nLSU+RPB1+RPB2+TEF1 sequence matrix, and *Bjerkandera adusta* (Willd.) P. Karst. was used as an outgroup for phylogenetic analysis of the phylogenetic tree (Fig. 1). And *Byssomerulius corium* (Pers.) Parmasto was used as an outgroup for phylogenetic analysis of the ITS+nLSU+RPB1+RPB2+TEF1 phylogenetic tree (Fig. 2). To determine the phylogeny, we compiled an ITS+nLSU+RPB1+RPB2+TEF1 sequence matrix, and *Hyphoderma setigerum* (Fr.) Donk was used as an outgroup for phylogenetic analysis of the phylogenetic tree (Fig. 3). And *Climacodon septentrionalis* (Fr.) P. Karst. was used as an outgroup for phylogenetic analysis of the ITS+nLSU+RPB2+TEF1 phylogenetic tree (Fig. 4).

Table 1. List of species, specimens and GenBank accession numbers of sequences used in this study. [New species is in bold; * is type material, holotype].

Species name	Specimen No.	GenBank accession No.					Country	References
		ITS	nLUS	*rpb1*	*rpb2*	*tef1-α*		
Allophlebia formosana	He 3805	PP549545	PP549577	—	—	—	China	Li et al. (2025)
Allophlebia formosana	He 4394	PP549546	PP549578	—	—	—	China	Li et al. (2025)
Aurantiopileus mayanensis	JV 1504/128	KT156706	—	—	—	—	Costa Rica	Zhao et al. (2023)
Aurantiopileus mayanensis	TJB10228	HM772140	HM772139	—	—	—	Belize	Ginns et al. (2010)
Aurantiporus venustus	391/12	OL630489	OL635577	—	—	—	Brazil	Unpublished
Bjerkandera adusta	HHB-12826-Sp	KP134983	KP135198	—	—	—	USA	El-Gharabawy et al. (2021)
Bjerkandera adusta	MUT<ITA>:5195	KM355986	MF115840	—	—	—	Italy	El-Gharabawy et al. (2021)
Byssomerulius corium	FP-102382	KP135007	KP135230	KP134802	KP134921	—	USA	Floudas and Hibbett (2015)
Byssomerulius corium	WEI 17-645	LC427006	LC427030	—	—	—	China	Chen et al. 2020
Candelabrochaete guangdongensis	He 5902	MZ422527	MZ422499	—	—	—	China	Li et al. (2022)
Ceriporia mellita	GC 1508-71	LC427022	LC427044	—	—	—	China	Chen et al. (2021)
Ceriporia mellita	WEI 17-024	LC427024	LC427046	—	—	—	China	Chen et al. (2021)
Ceriporia viridans	GC 1708-211	LC427027	LC427049	LC427062	—	—	China	Chen et al. (2021)
Ceriporia viridans	Miettinen 11701	KX752600	KX752600	—	—	—	Netherlands	Miettinen et al. (2016)
Ceriporiopsis tianshanensis	Cui 19150	OP920992	OP920984	—	—	—	China	Xu et al. (2023)
Ceriporiopsis tianshanensis	Cui 19151	OP920993	OP920985	—	—	—	China	Xu et al. (2023)
Ceriporiopsoides guidella	HUBO 7659	FJ496687	FJ496722	—	—	—	Italy	Tomšovský et al. (2010)
Ceriporiopsoides lagerheimii	58240	KX008365	KX081077	—	—	—	China	Zhao et al. (2017)
Ceriporiopsoides lagerheimii	Dai 12304	KX161647	KX161651	—	—	—	China	Zhao et al. (2023)
Climacodon septentrionalis	AFTOL-767	AY854082	AY684165	AY864873	AY780941	AY885151	USA	Lutzoni et al. (2004)
Climacodon septentrionalis	RLG-6890-Sp	KP135344	—	—	—	—	USA	Floudas and Hibbett (2015)
Crustodontia chrysocreas	HHB-6333-Sp	KP135358	KP135263	KP134861	KP134908	—	USA	Floudas and Hibbett (2015)
Crustodontia nigrodontea	CLZhao 2758	MT896824	—	—	—	—	China	Huang et al. (2020)
Crystallicutis albomarginata	**CLZhao 31409**	**PV470538**	**PV474183**	—	—	**PV759048**	**China**	**Present study**
Crystallicutis albomarginata	**CLZhao 31506 ***	**PV470539**	**PV474184**	—	**PV759033**	**PV759049**	**China**	**Present study**
Crystallicutis damiettensis	UN63A	KX428470	MW508515	MW523003	—	MW523002	Egypt	El-Gharabawy et al. (2016)
Crystallicutis huangshanensis	Dai 6090	JX623934	JX644066	—	—	—	China	El-Gharabawy et al. (2021)
Crystallicutis rajchenbergii	MR-4310	KY948797	KY948888	KY948963	—	—	USA	Justo et al. (2017)
Crystallicutis serpens	HHB-15692-Sp	KP135031	KP135200	KP134785	KP134914	—	USA	Floudas and Hibbett (2015)
Crystallicutis serpens	TNM:F30569	MZ636946	—	—	—	—	China	Chen et al. (2021)
Cytidiella albomarginata	He 5575	MZ422526	MZ422497	—	—	—	China	Li et al. (2022)
Cytidiella albomarginata	WEI 18-474	MZ636948	MZ637110	—	—	—	China	Chen et al. (2021)
Cytidiella nitidula	He 5126	MZ422523	MZ422494	—	—	—	China	Li et al. (2022)
Cytidiella nitidula	He 5135	MZ422524	MZ422495	—	—	—	China	Li et al. (2022)
Efibula americana	HHB-10209-Sp	KP135014	—	—	—	—	USA	Floudas and Hibbett (2015)
Efibula americana	FP-102165	KP135016	KP135256	KP134808	KP134916	MZ913669	USA	Floudas and Hibbett (2015)
Efibula americana	HHB-8468	KP135012	—	—	—	—	USA	Floudas and Hibbett (2015)
Efibula clarkii	FD-228	KP135019	—	KP134803	—	—	USA	Floudas and Hibbett (2015)
Efibula cordylines	ICMP 18129	PQ214293	—	—	—	—	New Zealand	Unpublished
Efibula daweishanensis	CLZhao 18946	OR094488	—	—	—	OR541912	China	Dong et al. (2024)
Efibula daweishanensis	CLZhao 19002	OR094489	OR449958	—	—	—	China	Dong et al. (2024)
Efibula daweishanensis	CLZhao 25072	OR094490	OR449959	—	OR733284	OR541913	China	Dong et al. (2024)
Efibula glossophora	**CLZhao 22744 ***	**PV470540**	**PV474185**	**PV747409**	**PV759036**	**PV759050**	**China**	**Present study**
Efibula gracilis	FD-455	KP135027	MZ637116	KP134804	OK136077	MZ913679	USA	Chen et al. (2021)
Efibula gracilis	FP-102052	KP135028	—	—	—	—	USA	Floudas and Hibbett (2015)
Efibula grandinosa	He 6312	MZ422509	MZ422480	—	—	—	China	Li et al. (2022)
Efibula hainanensis	He 6004	MW580949	MW580939	—	—	—	China	Li et al. (2022)
Efibula hainanensis	Chen 1284	ON117184	—	—	—	—	China	Li et al. (2022)

Species name	Specimen No.	GenBank accession No.					Country	References
		ITS	nLUS	*rpb1*	*rpb2*	*tef1-α*		
Efibula intertexta	Wu 1707-93	MZ636953	MZ637117	MZ748416	OK136085	—	China	Chen et al. (2021)
Efibula intertexta	Wu 1707-96	MZ636954	MZ637118	MZ748417	OK136086	—	China	Chen et al. (2021)
Efibula matsuensis	Wu 1011-18	MZ636956	MZ637119	MZ748418	OK136078	MZ913680	China	Chen et al. (2021)
Efibula matsuensis	Wu 1011-19	MZ636957	MZ637120	—	—	—	China	Chen et al. (2021)
Efibula punctata	**CLZhao 22764**	**PV470541**	**PV474186**	**PV747410**	**PV759037**	**PV759051**	**China**	**Present study**
Efibula punctata	**CLZhao 29674**	**PV470542**	**PV474187**	—	**PV759038**	**PV759052**	**China**	**Present study**
Efibula punctata	**CLZhao 29678**	**PV470543**	**PV474188**	**PV747411**	**PV759039**	**PV759053**	**China**	**Present study**
Efibula punctata	**CLZhao 30011 ***	**PV470544**	**PV474189**	—	**PV759040**	**PV759054**	**China**	**Present study**
Efibula punctata	**CLZhao 30054**	**PV470545**	**PV474190**	**PV747412**	**PV759041**	**PV759055**	**China**	**Present study**
Efibula punctata	**CLZhao 30615**	**PV470546**	**PV474191**	—	—	**PV759056**	**China**	**Present study**
Efibula punctata	**CLZhao 30637**	**PV470547**	**PV474192**	**PV747413**	**PV759042**	**PV759057**	**China**	**Present study**
Efibula punctata	**CLZhao 30648**	**PV470548**	**PV474193**	—	**PV759043**	**PV759058**	**China**	**Present study**
Efibula punctata	**CLZhao 30659**	**PV470549**	**PV474194**	**PV747414**	**PV759044**	**PV759059**	**China**	**Present study**
Efibula punctata	**CLZhao 30664**	**PV470550**	**PV474195**	**PV747415**	**PV759045**	**PV759060**	**China**	**Present study**
Efibula punctata	**CLZhao 30691**	**PV470551**	**PV474196**	**PV747416**	**PV759046**	**PV759061**	**China**	**Present study**
Efibula punctata	**CLZhao 30718**	**PV470552**	**PV474197**	**PV747417**	**PV759047**	**PV759062**	**China**	**Present study**
Efibula shenghuae	He 3384	MZ422508	MZ422479	—	—	—	China	Li et al. (2022)
Efibula subglobispora	He 3983	MW580944	MW580934	—	—	—	China	Li et al. (2022)
Efibula subglobispora	He 7032	MZ422506	MZ422477	—	—	—	China	Li et al. (2022)
Efibula subglobispora	Chen 1716	MZ636962	MZ637124	MZ748427	OK136075	MZ913673	China	Chen et al. (2021)
Efibula subglobispora	GC 1604-13	MZ636963	MZ637125	MZ748428	OK136076	MZ913674	China	Chen et al. (2021)
Efibula taiwanensis	He 4582	MZ422507	MZ422478	—	—	—	China	Li et al. (2022)
Efibula tropica	WEI 18-149	MZ636967	MZ637129	MZ748419	OK136079	MZ913681	China	Chen et al. (2021)
Efibula tropica	Wu 0809-8	MZ636968	MZ637130	—	—	—	China	Chen et al. (2021)
Efibula tuberculata	Wu 1005-55	MZ636970	MZ637132	MZ748426	OK136074	MZ913672	China	Chen et al. (2021)
Efibula tuberculata	Wu 0711-148	MZ636969	MZ637131	—	—	MZ913671	China	Chen et al. (2021)
Efibula turgida	Wu 0910-86	MZ636972	MZ637134	MZ748439	OK136091	MZ913716	China	Chen et al. (2021)
Efibula turgida	Wu 0910-99	MZ636973	MZ637135	MZ748440	OK136092	MZ913717	China	Chen et al. (2021)
Efibula yunnanensis	He 4653	MW580948	MW580938	—	—	—	China	Li et al. (2022)
Efibula yunnanensis	He 6970	MZ422505	MZ422476	—	—	—	China	Li et al. (2022)
Efibula yunnanensis	Wu 880515-1	MZ636977	GQ470672	MZ748420	OK136080	MZ913682	China	Chen et al. (2021)
Efibula yunnanensis	CLZhao 11641	MT611529	—	—	—	—	China	Ma et al. (2020)
Flavodon ambrosius	HULCR-6860	KR119074	KR119077	—	—	—	USA	El-Gharabawy et al. (2021)
Flavodon flavus	LE295997	KF856505	KF856510	—	—	—	Tanzania	Zmitrovich and Malysheva (2014)
Flavodon flavus	WHC 1381	LC427029	LC427052	—	—	—	China	Chen et al. (2021)
Geesterania carneola	MCW 388/12	KY174999	KY174999	—	KY175011	KY175013	Brazil	Westphalen et al. (2018)
Geesterania davidiae	MCW 396/12	KY174998	KY174998	—	KY175012	KY175016	Brazil	Westphalen et al. (2018)
Gloeoporus hainanensis	Yuan-4397	KU360400	KU360409	—	—	—	China	El-Gharabawy et al. (2021)
Gloeoporus pannocinctus	L-15726-Sp	KP135060	KP135214	KP134867	KP134973	—	USA	El-Gharabawy et al. (2021)
Hermanssonia centrifuga	CBS 125890	MH864088	MH875547	—	—	—	Sweden	Vu et al. (2019)
Hermanssonia centrifuga	HHB-9239-Sp	KP135380	KP135262	KP134844	KP134974	MZ913721	USA	Floudas and Hibbett (2015)
Hermanssonia fimbriata	Dai 23266	ON135436	ON135440	—	—	—	China	Liu et al. (2022)
Hermanssonia fimbriata	Dai 23305	ON135437	ON135441	—	—	—	China	Liu et al. (2022)
Hydnophanerochaete odontoidea	CLZhao 3882	MH784919	MH784929	—	—	—	China	Shen et al. (2018)
Hydnophanerochaete odontoidea	CLZhao 4036	MH784927	MH784937	—	—	—	China	Shen et al. (2018)
Hydnophlebia acanthocystis	FP 150571	KY948767	KY948844	KY948914	—	—	USA	Justo et al. (2017)
Hydnophlebia chrysorhiza	FD-282	KP135338	KP135217	KP134848	KP134897	—	USA	Floudas and Hibbett (2015)
Hydnophlebia chrysorhiza	HHB-18767	KP135337	—	—	—	—	USA	Floudas and Hibbett (2015)
Hydnophlebia gorgonea	MA-Fungi 86642	KF483031	KF528122	—	—	—	Cape Verde	Telleria et al. (2017)
Hyphoderma setigerum	FD-312	KP135297	KP135222	KP134871	—	—	USA	Floudas and Hibbett (2015)
Irpex alboflavescens	He 3933	MZ422503	MZ422474	—	—	—	China	Li et al. (2022)

Species name	Specimen No.	GenBank accession No.					Country	References
		ITS	nLUS	*rpb1*	*rpb2*	*tef1-α*		
Irpex alboflavescens	He 4719	MZ422501	MZ422472	—	—	—	China	Li et al. (2022)
Irpex latemarginatus	FP-55521T	KP135024	KP135202	KP134805	KP134915	—	USA	Floudas and Hibbett (2015)
Irpex latemarginatus	Piatek 1997	KX752592	KX752592	—	—	—	Poland	Miettinen et al. (2016)
Irpex rosea	He 6277	MW580943	MW580933	—	—	—	China	Li et al. (2022)
Irpex rosea	CLZhao 18491	MW377575	MW377578	—	—	—	China	Wang and Zhao (2022)
Leptoporus mollis	RLG-7163	KY948794	—	KY948956	—	—	USA	Justo et al. (2017)
Leptoporus mollis	TJV_93_174T	KY948795	EU402510	KY948957	—	—	USA	Justo et al. (2017)
Lilaceophlebia tremelloidea	Bosco_Siro_ Negri_1	PP716904	PP716909	—	—	—	Italy	Girometta et al. (2025)
Lilaceophlebia tremelloidea	Bosco_Siro_ Negri_2	PP716903	PP716910	—	—	—	Italy	Girometta et al. (2025)
Luteochaete subglobosa	CLZhao 3639	MK881898	MK881788	—	—	—	China	Huang et al. (2020)
Luteochaete subglobosa	CLZhao 3475	MK881897	MK881787	—	—	—	China	Huang et al. (2020)
Luteoporia albomarginata	GC 1702-1	LC379003	LC379155	LC379160	LC387358	LC387377	China	Wu et al. (2016)
Luteoporia citriniporia	Dai 19507	MT872218	MT872216	—	—	—	China	Liu and Yuan (2020)
Luteoporia straminea	CLZhao 18947	MW732407	MW724799	—	—	—	China	Zhao et al. (2023)
Meruliopsis crassitunicata	CHWC 1506-46	LC427010	LC427034	—	—	—	China	Chen et al. (2021)
Meruliopsis leptocystidiata	Wu 1708-43	LC427013	LC427033	—	—	—	China	Chen et al. (2021)
Meruliopsis parvispora	Wu 1209-58	LC427017	LC427039	—	—	—	China	Chen et al. (2021)
Meruliopsis taxicola	GC 1704-60	LC427028	LC427050	—	—	—	China	Chen et al. (2021)
Merulius nantahaliensis	HHB-2816-sp	KY948777	KY948852	KY948920	—	—	USA	Justo et al. (2017)
Merulius sinensis	CLZhao 2562	MW732401	MW724793	—	—	—	China	Zhao et al. (2023)
Mycoacia aurea	DLL 2011-263	KJ140747	—	—	—	—	USA	Binder et al. (2005)
Mycoacia aurea	RLG 5075sp	KY948759	MZ637161	KY948918	—	—	USA	Binder et al. (2005)
Mycoacia kunmingensis	CLZhao 152	KX081072	KX081074	—	—	—	China	Zhao and Wu (2017)
Mycoacia kunmingensis	CLZhao 153	KX081073	KX081075	—	—	—	China	Zhao and Wu (2017)
Mycoaciella efibulata	WEI 19-057	MZ637012	MZ637172	—	—	—	China	Chen et al. (2021)
Mycoaciella efibulata	WEI 16-172	MZ637011	MZ637171	—	—	—	China	Chen et al. (2021)
Odoria alborubescens	BP 106943	MG097864	MG097867	—	—	—	Hungary	Papp and Dima (2017)
Odoria alborubescens	BRNU 627479	JQ821319	JQ821318	—	—	—	Czech Republic	Dvoˇrák et al. (2014)
Pappia fissilis	BRNM 699803	HQ728292	HQ729002	—	—	—	Czech Republic	Tomšovský (2012)
Pappia fissilis	814	HQ728291	HQ729001	—	—	—	Czech Republic	Tomšovský (2012)
Phanerochaetella formosana	He 3391	MZ422520	MZ422491	—	—	—	China	Li et al. (2022)
Phanerochaetella formosana	He 3962	MZ422522	MZ422493	—	—	—	China	Li et al. (2022)
Phanerochaetella queletii	He 3050	MZ422512	MZ422483	—	—	—	China	Li et al. (2022)
Phanerochaetella queletii	He 3284	MZ422510	MZ422481	—	—	—	China	Li et al. (2022)
Phlebia acerina	FD 301	KP135378	—	KP134862	—	—	USA	Justo et al. (2017)
Phlebia acerina	HHB 11146	KP135372	—	—	—	—	USA	Floudas and Hibbett (2015)
Phlebia floridensis	HHB-9905-sp	KP135383	KP135264	KP134863	KP134899	—	USA	Floudas and Hibbett (2015)
Phlebia radiata	CBS 285.56	MH857642	MH869187	—	—	—	France	Vu et al. (2019)
Phlebia rufa	FBCC297	LN611092	LN611092	—	—	—	Finland	Kuuskeri et al. (2015)
Phlebia rufa	HHB-14924	KP135374	—	—	—	—	USA	Floudas and Hibbett (2015)
Phlebicolorata alboaurantia	Cui 4136	KF845955	KF845948	—	—	—	China	Zhao and Cui (2014)
Phlebicolorata pseudoplacenta	Miettinen 18997	KY948744	KY948902	KY948926	—	—	USA	Justo et al. (2017)
Phlebiodontia caspica	FCUG 3159	HQ153410	—	—	—	—	Iran	Ghobad-Nejhad and Hallenberg (2012)
Phlebiodontia fissurata	EM 13468	OR822135	—	—	—	—	Switzerland	Larsson et al. (2025)
Phlebiporia bubalina	Dai 13168	KC782526	KC782528	—	—	—	China	Chen and Cui (2014)
Phlebiporia bubalina	Dai 15179	KY131843	KY131902	—	—	—	China	Wu et al. (2017)
Physisporinus vitreus	Larsson 11959	JN710580	JN710580	—	—	—	Norway	Miettinen et al. (2012)

Species name	Specimen No.	GenBank accession No.					Country	References
		ITS	nLUS	*rpb1*	*rpb2*	*tef1-α*		
Physisporinus yunnanensis	CLZhao 21583	OP852341	OP852343	—	—	—	China	Cai et al. (2023)
Physisporinus yunnanensis	CLZhao 21647	OP852340	OP852342	—	—	—	China	Cai et al. (2023)
Pseudonadsoniella brunnea	KTA-37	KT456204	—	—	—	—	Argentina	Kondratyuk et al. (2015)
Pseudophlebia setulosa	HHB-6891-Sp	KP135382	KP135267	KP134864	KP134901	MZ913650	USA	Zong and Zhao (2021)
Pseudophlebia setulosa	PH 11749	GU461312	GU461312	—	—	—	Spain	Moreno et al. (2011)
Raduliporus aneirinus	HHB-15629-Sp	KP135023	KP135207	KP134795	—	—	USA	Floudas and Hibbett (2015)
Resiniporus resinascens	BRNM 710169	FJ496675	FJ496698	—	—	—	Czech Republic	Tomšovský et al. (2010)
Sarcodontia amplissima	CFMR:FP-104176	MZ322829	MZ322839	—	—	—	USA	Nakasone et al. (2021)
Sarcodontia amplissima	CFMR:FP-101997	MZ322828	MZ322838	—	—	—	USA	Nakasone et al. (2021)
Scopuloides allantoidea	GC 1602-11	MZ637080	MZ637278	—	—	—	China	Chen et al. (2021)
Scopuloides allantoidea	WEI 16-060	MZ637081	MZ637279	—	OK136047	MZ913664	China	Chen et al. (2021)
Scopuloides dimorpha	FP-102935-Sp	KP135353	KP135285	KP134855	KP134905	—	USA	Zong and Zhao (2021)
Scopuloides dimorpha	WEI 19-073	MZ637084	MZ637282	—	—	—	China	Chen et al. (2021)
Scopuloides ellipsoidea	He 4681	PP549568	PP549602	—	—	—	China	Li et al. (2025)
Scopuloides ellipsoidea	He 4760	PP549569	PP549603	—	—	—	China	Li et al. (2025)
Scopuloides farinacea	**CLZhao 30005**	**PV470558**	**PV474203**	**—**	**PV759034**	**PV763684**	**China**	**Present study**
Scopuloides farinacea	**CLZhao 30181 ***	**PV470559**	**PV474204**	**—**	**—**	**PV763685**	**China**	**Present study**
Scopuloides farinacea	**HMZhou 153**	**PV470560**	**PV474205**	**—**	**PV759035**	**PV763686**	**China**	**Present study**
Scopuloides grandinioides	He 6295	PP549571	PP549605	—	PP566657	—	China	Li et al. (2025)
Scopuloides grandinioides	RLG-5104-sp	KP135351	KP135283	—	KP134904	—	USA	Li et al. (2025)
Scopuloides hydnoides	FP-150473	KP135355	KP135284	KP134854	—	—	USA	Zong and Zhao (2021)
Scopuloides hydnoides	He 4507	PP549572	PP549606	—	—	—	China	Li et al. (2025)
Scopuloides leprosa	FRDBI 17584773	MW487975	—	—	—	—	UK	Unpublished
Scopuloides rimosa	HHB-7042-Sp	KP135350	KP135282	KP134853	KP134903	—	USA	Zong and Zhao (2021)
Scopuloides rimosa	He 3320	PP549574	PP549608	—	—	—	China	Li et al. (2025)
Scopuloides rimosa	He 3620	PP549575	PP549609	—	—	—	China	Li et al. (2025)
Scopuloides yunnanensis	CLZhao 18588	PP511312	PP511315	—	—	—	China	Gu et al. (2024)
Scopuloides yunnanensis	CLZhao 30079	PP511313	PP511316	—	—	—	China	Gu et al. (2024)
Scopuloides yunnanensis	CLZhao 30213	PP511314	PP511317	—	—	—	China	Gu et al. (2024)
Stereophlebia tuberculata	FCUG 3157	HQ153427	—	—	—	—	Iran	Ghobad-Nejhad and Hallenberg (2012)
Stereophlebia tuberculata	Wu 1708-107	MZ637089	MZ637286	—	—	—	China	Chen et al. (2021)
Trametopsis aborigena	Robledo 1236	KY655336	KY655338	—	—	—	Argentina	Gómez-Montoya et al. (2017)
Trametopsis cervina	TJV-93-216T	JN165020	JN164796	JN164839	JN164877	JN164882	USA	Justo and Hibbett (2011)

Maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference (BI) analyses were applied to the combined four datasets. The approach followed the previous study by Yang et al. (2025a) and Qin et al. (2025), and the tree construction procedure was performed in PAUP* version 4.0a169 (Swofford 2002; Yang et al. 2025b). All characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1,000 random sequence additions. Max-trees were set to 5,000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 replicates. Descriptive tree statistics—tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI)—were calculated for each maximum parsimonious tree generated. The combined dataset was also analyzed using ML in RAxML-HPC2 through the Cipres Science Gateway. Branch support (BS) for ML analysis was determined by 1,000 bootstrap replicates (Wang et al. 2024; Yang et al. 2025a).

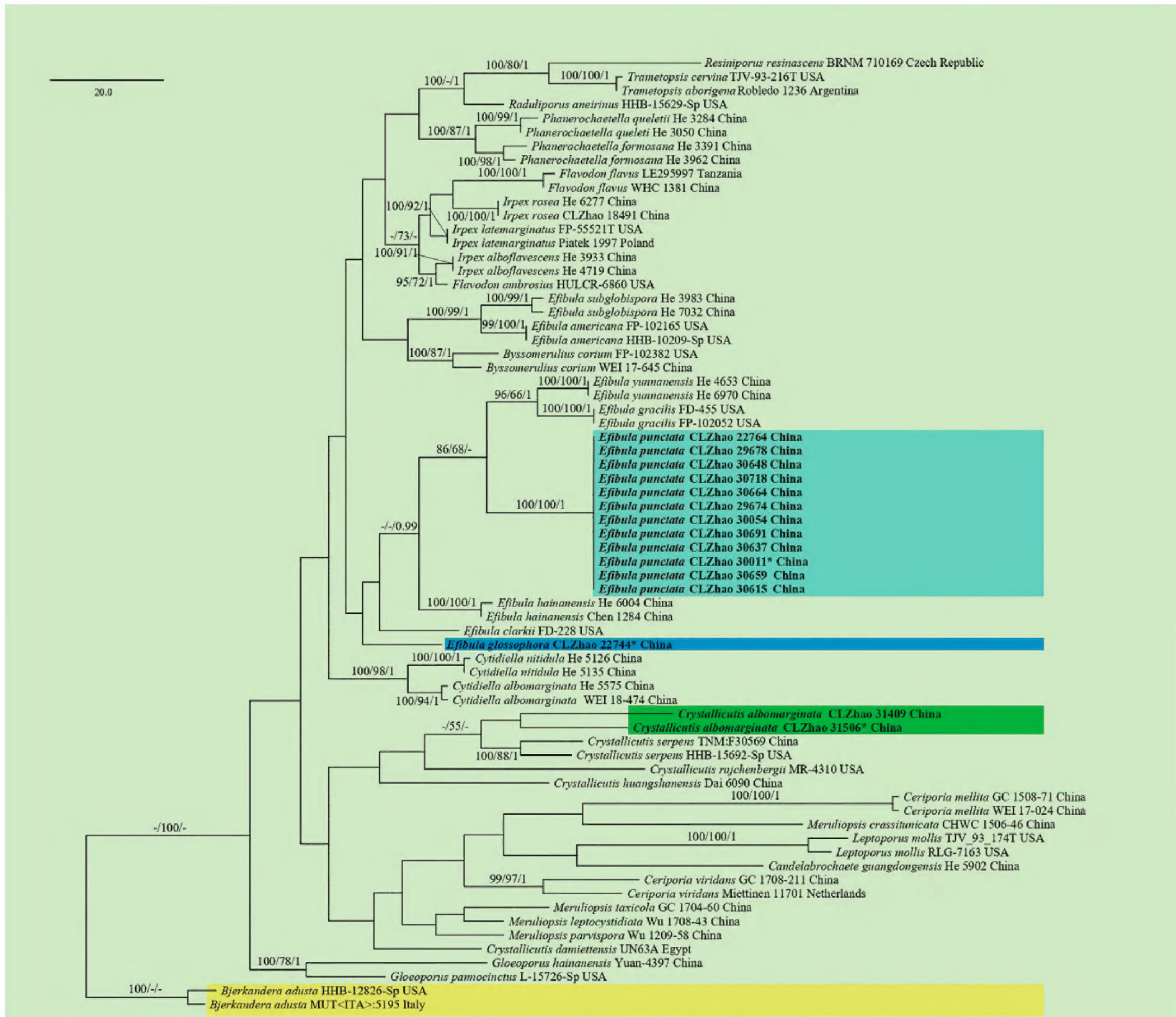

Figure 1. Maximum parsimony strict consensus tree illustrating the phylogenetic relationships of the three new species and related species within the family Irpicaceae based on ITS+nLSU+RPB1+RPB2+TEF1 sequences. Branches are labelled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95. The new species is in bold.

The best evolutionary model of each alignment was estimated using jModelTest (Guindon and Gascuel 2003; Posada 2008) under the Akaike information criterion. MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for the dataset for Bayesian inference (BI). BI was calculated with MrBayes version 3.2.7a (Ronquist et al. 2012). Four Markov chains were run for 2 runs from random starting trees for 1.45 million generations for ITS+nLSU+RPB1+RPB2+TEF1 (Fig. 1). Four Markov chains were run for 2 runs from random starting trees for 500 thousand generations for ITS+nLSU+RPB1+RPB2+TEF1 (Fig. 2). Four Markov chains were run for 2 runs from random starting trees for 2.42 million generations for ITS+nLSU+RPB1+RPB2+TEF1 (Fig. 3). Four Markov chains were run for 2 runs from random starting trees for 500 thousand generations for ITS+nLSU+RPB2+TEF1 (Fig. 4). The first one-fourth of all generations was discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were

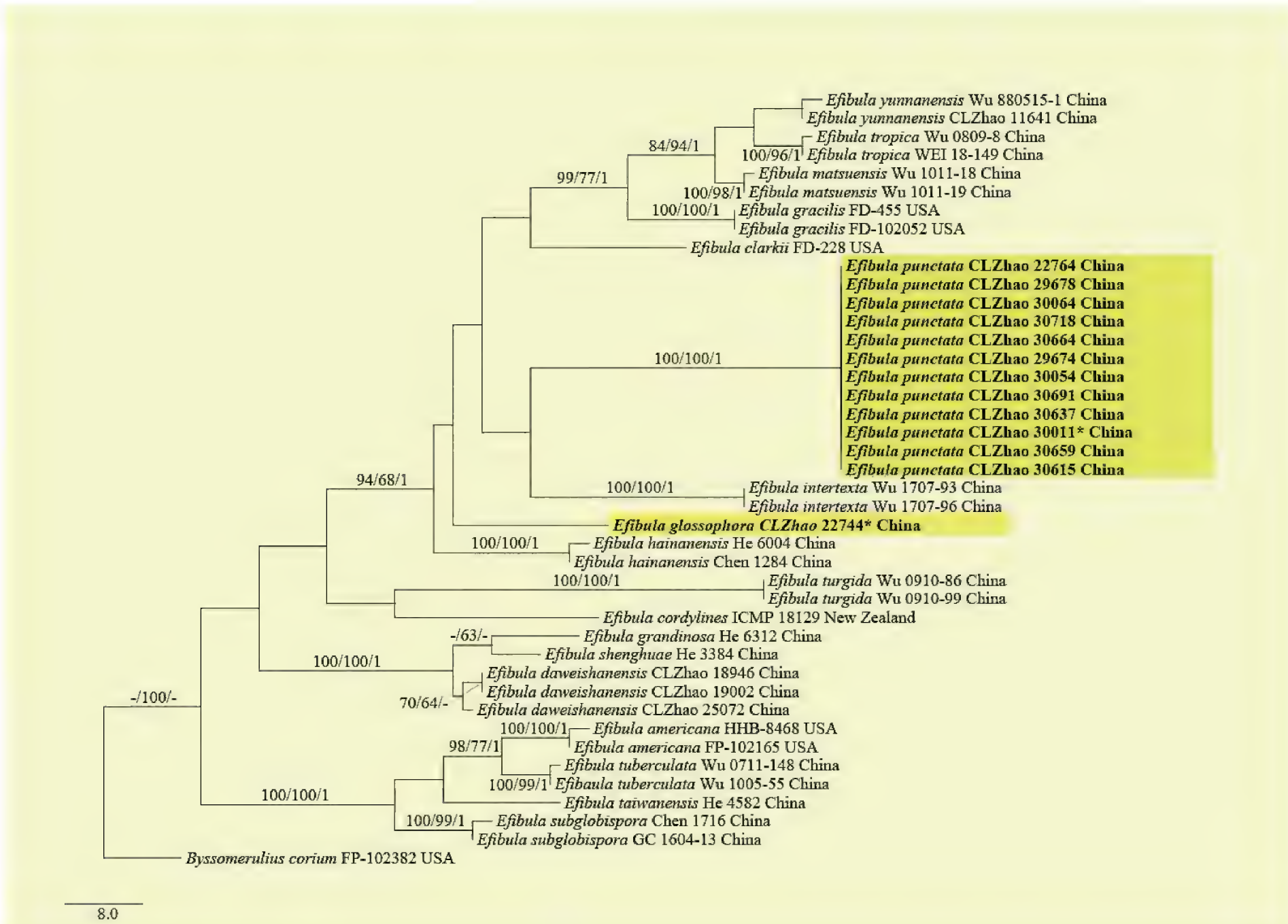

Figure 2. Maximum parsimony strict consensus tree illustrating the phylogenetic relationships of the three new species and related species in *Efibula* based on ITS+nLSU+RPB1+RPB2+TEF1 sequences. Branches are labelled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95. The new species is in bold.

considered as significantly supported if they received a maximum likelihood bootstrap value (BS) > 70%, a maximum parsimony bootstrap value (BT) > 50%, or Bayesian posterior probabilities (BPP) > 0.95.

Results

Molecular phylogeny

In Irpicaceae analyses, the ITS+nLSU+RPB1+RPB2+TEF1 dataset (Fig. 1) included sequences from 69 fungal specimens representing 38 taxa. The dataset had an aligned length of 5047 characters, of which 3162 characters are constant, 492 are variable and parsimony-uninformative, and 1393 are parsimony-informative. Maximum parsimony analysis yielded 4 equally parsimonious trees (TL = 1226, CI = 0.3100, HI = 0.6900, RI = 0.5925, and RC = 0.1836). The best model for the ITS+nLSU+RPB1+RPB2+TEF1 dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as in the MP analysis, with an average standard deviation of split frequencies = 0.009515 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg ESS = 640).

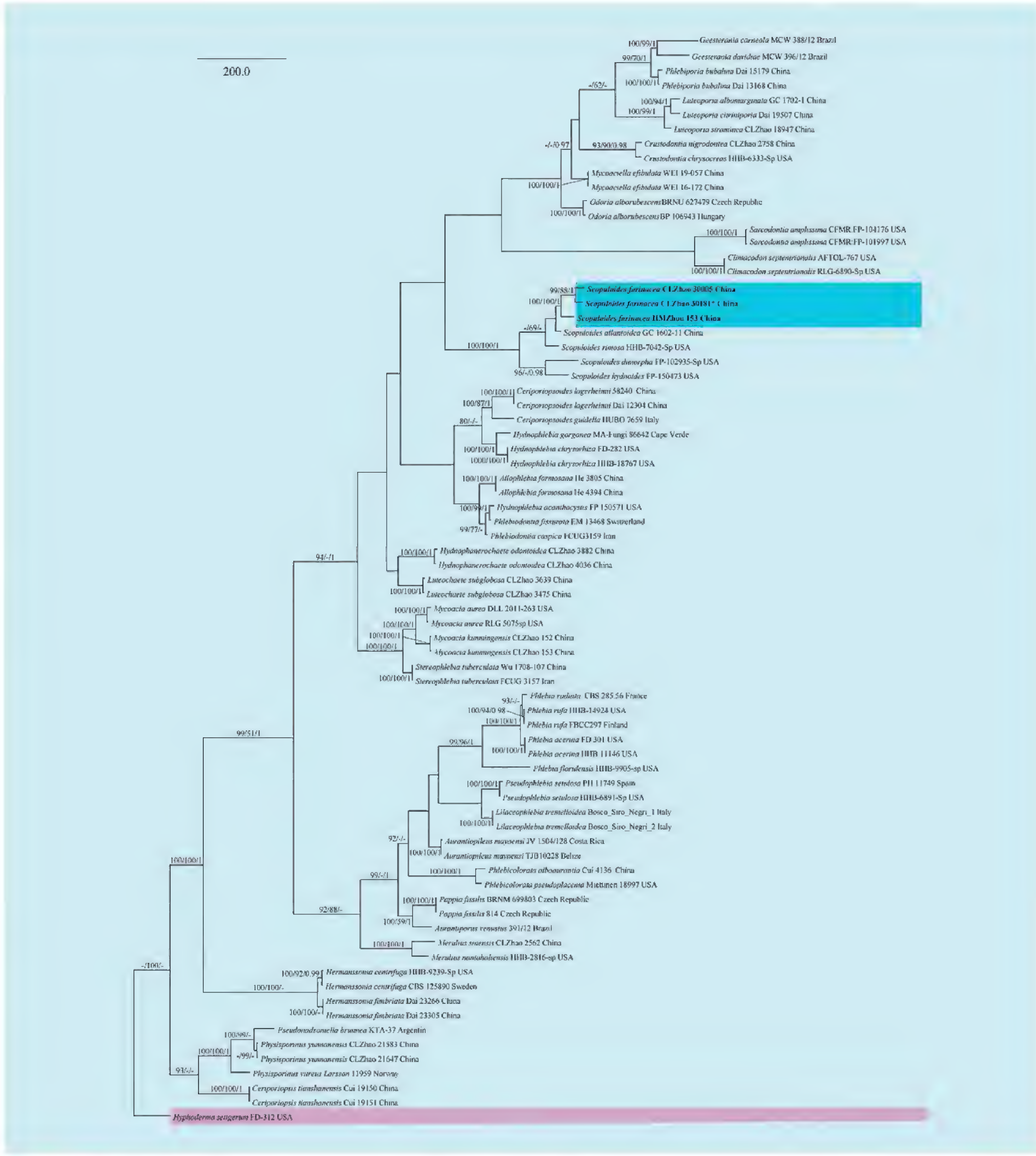
200.0
Geesteranta carneola MCW 388/12 Brazil
Geesteranta davidae MCW 396/12 Brazil
Phlebiporia bubalina Dai 15179 China
Phlebiporia bubalina Dai 13168 China
Luteoporia albomarginata GC 1702-1 China
Luteoporia citriniporia Dai 19507 China
Luteoporia straminea CLZhao 18947 China
Crustodontia nigrodontea CLZhao 2758 China
Crustodontia chrysocreas HHB-6333-Sp USA
Mycoacella efibulata WEI 19-057 China
Mycoacella efibulata WEI 16-172 China
Odoria alborubescens BRNU 627479 Czech Republic
Odoria alborubescens BP 106943 Hungary
Sarcodontia amphissima CFMR:FP-104176 USA
Sarcodontia amphissima CFMR:FP-101997 USA
Climacodon septentrionalis AFTOL-767 USA
Climacodon septentrionalis RLG-6890-Sp USA
Scopuloides farinacea CLZhao 30005 China
Scopuloides farinacea CLZhao 30181* China
Scopuloides farinacea HMZhou 153 China
Scopuloides atlantoidea GC 1602-11 China
Scopuloides rimosa HHB-7042-Sp USA
Scopuloides dimorpha FP-102935-Sp USA
Scopuloides hydnoides FP-150473 USA
Ceriporiopsoides lagerheimii 58240 China
Ceriporiopsoides lagerheimii Dai 12304 China
Ceriporiopsoides giuliella HUBO 7659 Italy
Hydnophlebia gorgonea MA-Fungi 86642 Cape Verde
Hydnophlebia chrysorhiza FD-282 USA
Hydnophlebia chrysorhiza HHB-18767 USA
Allophlebia formosana He 3805 China
Allophlebia formosana He 4394 China
Hydnophlebia acanthocystis FP 150571 USA
Phlebiodontia fissurata EM 13468 Switzerland
Phlebiodontia caspica FCUG3159 Iran
Hydnophanerochaete odontoidea CLZhao 3882 China
Hydnophanerochaete odontoidea CLZhao 4036 China
Luteochaete subglobosa CLZhao 3639 China
Luteochaete subglobosa CLZhao 3475 China
Mycoacia aurea DLL 2011-263 USA
Mycoacia aurea RLG 5075sp USA
Mycoacia kunmingensis CLZhao 152 China
Mycoacia kunmingensis CLZhao 153 China
Stereophlebia tuberculata Wu 1708-107 China
Stereophlebia tuberculata FCUG 3157 Iran
Phlebia radiata CBS 285.56 France
Phlebia rufa HHB-14924 USA
Phlebia rufa FBCC297 Finland
Phlebia acerina FD 301 USA
Phlebia acerina HHB 11146 USA
Phlebia floridensis HHB-9905-sp USA
Pseudophlebia setulosa PH 11749 Spain
Pseudophlebia setulosa HHB-6891-Sp USA
Lilaceophlebia tremelloidea Bosco_Siro_Negri_1 Italy
Lilaceophlebia tremelloidea Bosco_Siro_Negri_2 Italy
Aurantiopileus mayaensi JV 1504/128 Costa Rica
Aurantiopileus mayaensi TJD10228 Belize
Phlebicolorata alboaurantia Cui 4136 China
Phlebicolorata pseudoplacenta Miettinen 18997 USA
Pappia fissilis BRNM 699803 Czech Republic
Pappia fissilis 814 Czech Republic
Auriporus venustus 391/12 Brazil
Meruliusmenensis CLZhao 2562 China
Meruliusmantubaiensis HHB-2816-sp USA
Hermanssonia centrifuga HHB-9239-Sp USA
Hermanssonia centrifuga CBS 125890 Sweden
Hermanssonia fimbriata Dai 23266 China
Hermanssonia fimbriata Dai 23305 China
Pseudonadsonella brunnea KTA-37 Argentin
Physisporinus yunnanensis CLZhao 21583 China
Physisporinus yunnanensis CLZhao 21647 China
Physisporinus vitreus Larsson 11959 Norway
Ceriporiopsis tianshanensis Cui 19150 China
Ceriporiopsis tianshanensis Cui 19151 China
Hyphoderma setigerum FD-312 USA

Figure 3. Maximum parsimony strict consensus tree illustrating the phylogenetic relationships of the new species *Scopuloides farinacea* and related species within the family Meruliaceae based on ITS+nLSU+RPB1+RPB2+TEF1 sequences. Branches are labelled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95. The new species is in bold.

In *Efibula* analyses, the ITS+nLSU+RPB1+RPB2+TEF1 dataset (Fig. 2) included sequences from 42 fungal specimens representing 18 taxa. The dataset had an aligned length of 4694 characters, of which 3227 characters are constant, 225 are variable and parsimony-uninformative, and 1242 are parsimony-informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 409, CI = 0.5281, HI = 0.4719, RI = 0.8381, and RC

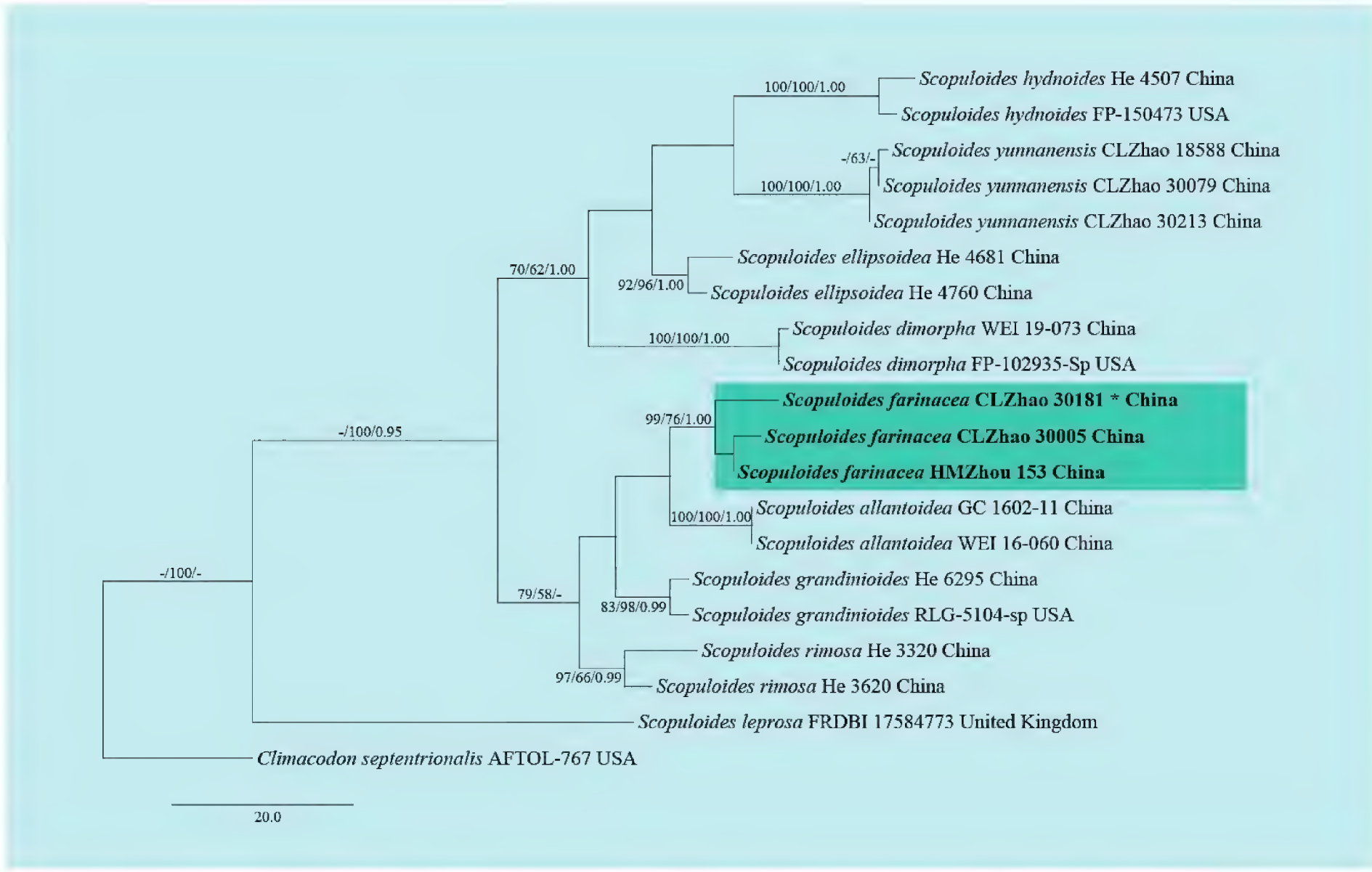

Figure 4. Maximum parsimony strict consensus tree illustrating the phylogenetic relationships of the new species *Scopuloides farinacea* and related species in *Scopuloides* based on ITS+nLSU+RPB2+TEF1 sequences. Branches are labelled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95. The new species is in bold.

= 0.4426). The best model for the ITS+nLSU+RPB1+RPB2+TEF1 dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as in the MP analysis, with an average standard deviation of split frequencies = 0.009147 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg ESS = 280).

In Irpicaceae analyses, the ITS+nLSU+RPB1+RPB2+TEF1 dataset (Fig. 3) included sequences from 75 fungal specimens representing 50 taxa. The dataset had an aligned length of 4958 characters, of which 2918 characters are constant, 659 are variable and parsimony-uninformative, and 1381 are parsimony-informative. Maximum parsimony analysis yielded 4 equally parsimonious trees (TL = 6725, CI = 0.4736, HI = 0.5264, RI = 0.5843, and RC = 0.2767). The best model for the ITS+nLSU+RPB1+RPB2+TEF1 dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as in the MP analysis, with an average standard deviation of split frequencies = 0.009989 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg ESS = 1010).

In *Scopuloides* analyses, the ITS+nLSU+RPB2+TEF1 dataset (Fig. 4) included sequences from 20 fungal specimens representing 10 taxa. The dataset had an aligned length of 3412 characters, of which 2813 characters are constant, 351 are variable and parsimony-uninformative, and 248 are parsimony-informative.

Maximum parsimony analysis yielded 13 equally parsimonious trees (TL = 314, CI = 0.6465, HI = 0.3535, RI = 0.7147, and RC = 0.4620). The best model for the ITS+nLSU+RPB2+TEF1 dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as in the MP analysis, with an average standard deviation of split frequencies = 0.009164 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg ESS = 454).

Based on the ITS+nLSU+RPB1+RPB2+TEF1 dataset (Fig. 1) of the family Irpicaceae, *Crystallicutis albomarginata* was sister to *C. serpens*. The ITS+nLSU+RPB1+RPB2+TEF1 dataset (Fig. 2) phylogenetic analysis of the genus *Efibula* showed that the two species were confirmed to be grouped together and clustered into the genus *Efibula*, in which *E. punctata* was sister to *E. intertexta* (Sheng H. Wu) C.C. Chen & Sheng H. Wu; *Efibula glossophora* is closely related to *E. intertexta* and *E. hainanensis* Yue Li & S.H. He. The phylogenetic analysis based on the ITS+nLSU+RPB1+RPB2+TEF1 dataset (Fig. 3) supported *Scopuloides farinacea* as a member of Meruliaceae, and based on the ITS+nLSU+RPB2+TEF1 dataset (Fig. 4) phylogenetic analysis, it was shown that the new species *S. farinacea* was sister to *S. allantoidea* C.C. Chen & Sheng H. Wu.

Taxonomy

***Crystallicutis albomarginata* Z.R. Gu & C.L. Zhao, sp. nov.**

MycoBank No: 858807

Figs 5–7

Diagnosis. Differs from other *Crystallicutis* species by its slightly pink to orange basidiomata when dry, a monomitic hyphal system with simple septa, and narrowly ellipsoid basidiospores measuring 3.7–4.4 × 1.9–2.8 µm.

Holotype. China • Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, GPS coordinates: 22°77'N, 104°29'E, altitude 1800 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 25 August 2023, CLZhao 31506, GenBank: ITS = PV470539, nLSU = PV474184 (SWFC).

Etymology. *Albomarginata* (Latin or Greek origin): refers to the white margin of the basidiomata.

Description. *Basidiomata*. Annual, resupinate, adnate, membranaceous, without odor or taste when fresh, up to 10 cm long, 2.5 cm wide, and 200 µm thick at center. Hymenial surface smooth, cream to pale pink when fresh, turning to slightly pink to orange upon drying. Sterile margin narrow, cream to pale pink, up to 1 mm.

***Hyphal system*.** Monomitic; generative hyphae with simple septa, colorless, thin- to slightly thick-walled, rarely branched, interwoven, 2.1–3 µm in diameter, IKI–, CB–; tissues unchanged in KOH. ***Hymenium*.** Cystidia fusiform, colorless, thin-walled, smooth, 12.5–27 × 3.5–6 µm. Basidia clavate, thin-walled, smooth, slightly flexuous, with four sterigmata and a simple septum at the base, 12.1–19.4 × 3.8–6 µm; basidioles in shape similar to basidia, but slightly smaller; subhymenial hyphae covered with smaller irregularly shaped colorless crystals. ***Basidiospores*.** Basidiospores narrowly ellipsoid, colorless, thin-walled, smooth, with 1-2 guttules, IKI–, CB–, (3.5–)3.7–4.4(–4.6) × (1.6–)1.9–2.8 µm, L = 4.06 µm, W = 2.33 µm, Q = 1.58–1.95 (n = 60/2).

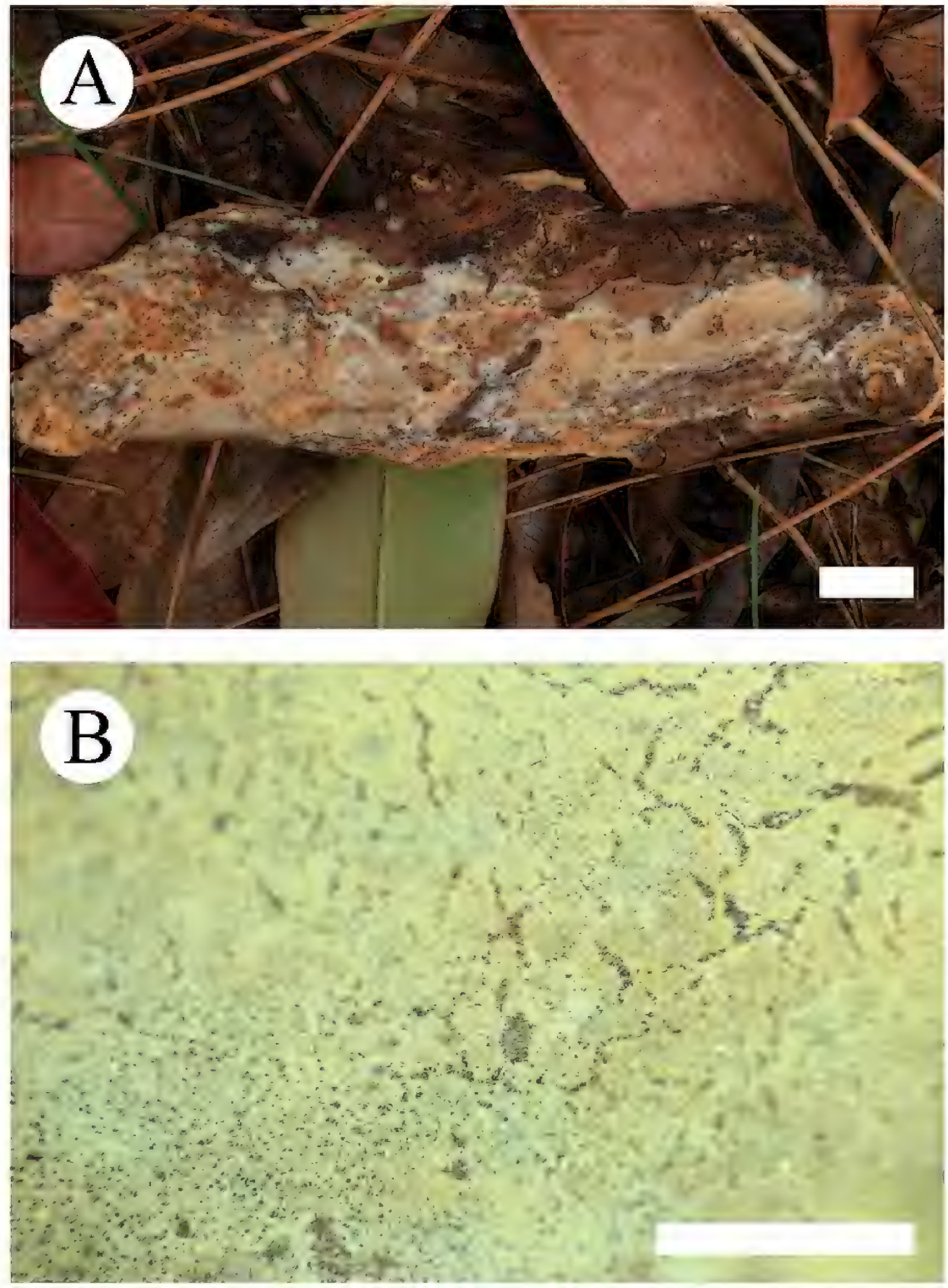

Figure 5. Basidiomata of *Crystallicutis albomarginata* (holotype, CLZhao 31506). **A.** Basidiomata on the substrate; **B.** Macroscopic characteristics of hymenophore. Scale bars: 1 cm (**A**); 1 mm (**B**).

Additional specimen examined (paratype). CHINA • Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, GPS coordinates: 22°77'N, 104°29'E, altitude 1800 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 25 August 2023, CLZhao 31409, GenBank: ITS = PV470538, nLSU = PV474183 (SWFC).

***Efibula glossophora* Z.R Gu & C.L. Zhao, sp. nov.**

MycoBank No: 858810

Figs 8–10

Diagnosis. Differs from other *Efibula* species by its hard, membranous, slightly yellow to yellow basidiomata; a monomitic hyphal system with simple-septa generative hyphae; and ellipsoid basidiospores measuring 3.8–6 × 2.6–3.7 µm.

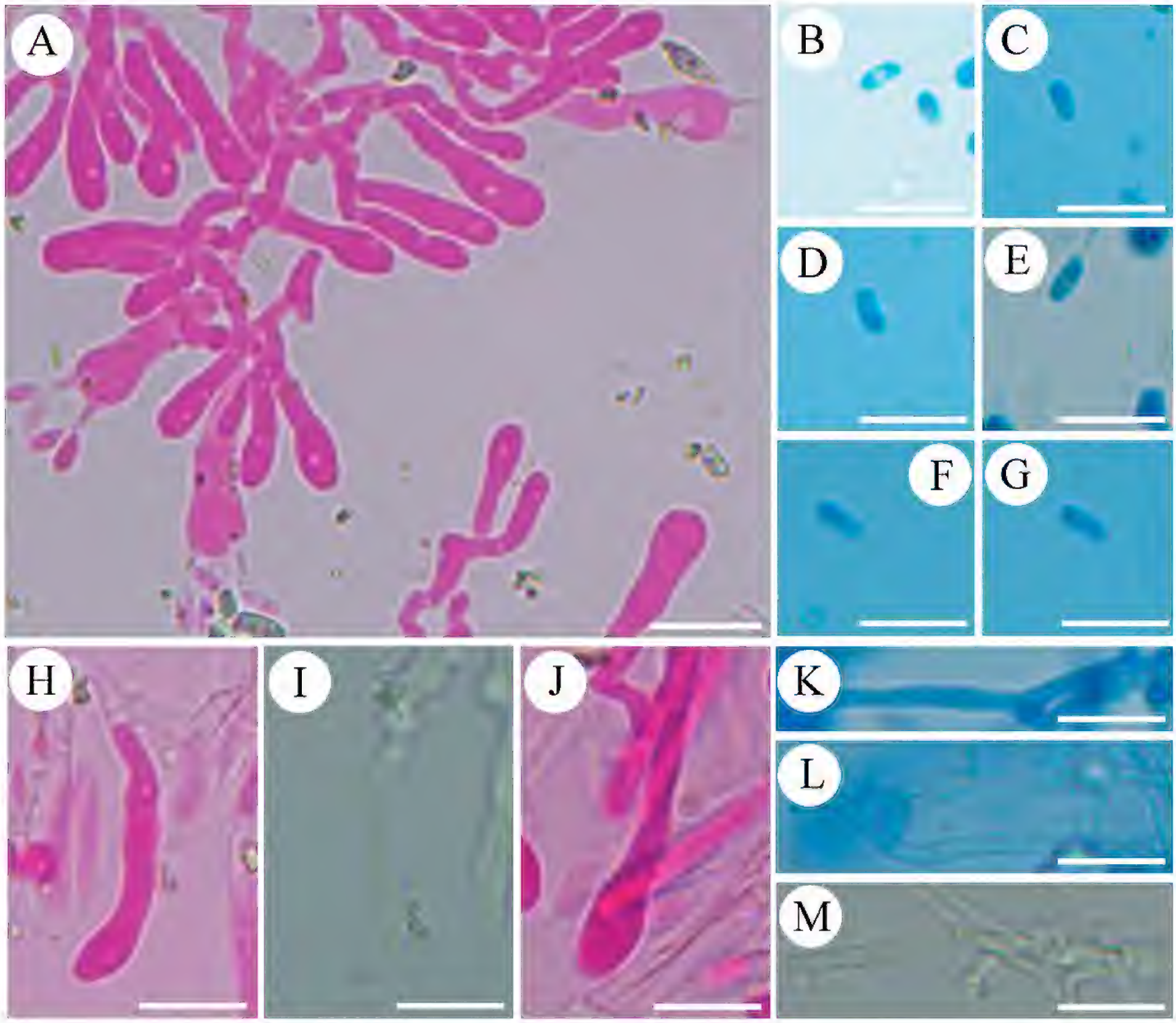

Figure 6. Sections of hymenium of *Crystallicutis albomarginata* (holotype, CLZhao 31506). **A.** Basidia and basidioles; **B–G.** Basidiospores; **H–J.** Cystidia; **K–M.** Part of the generative hyphae. Scale bars: 10 μm (**A–M**); 10 × 100 Oil.

Holotype. China • Yunnan Province, Dali, Weishan County, Leqiu Town, Zhongyao Village, GPS coordinates: 25°01'N, 100°4'E, altitude 1900 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 19 July 2022, CLZhao 22744, GenBank: ITS = PV470540, nLSU = PV474185 (SWFC).

Etymology. *Glossophora* (Latin or Greek origin): refers to the smooth hymenial surface of the type specimen.

Description. *Basidiomata*. Annual, resupinate, closely adnate, hard membranaceous, without odor or taste when fresh, up to 9 cm long, 2.5 cm wide, and 300 μm thick at center. Hymenophore smooth, buff to slightly yellow when fresh, slightly yellow to yellow upon drying. Sterile margin narrow, cream to slightly yellow, up to 1 mm.

***Hyphal system*.** Monomitic; generative hyphae with simple septa, colorless, thin- to slightly thick-walled, smooth, rarely branched, interwoven, 3–3.5 μm in diameter, IKI–, CB–; tissues unchanged in KOH. ***Hymenium*.** Cystidia and cystidioles absent. Basidia long clavate, slightly flexuous, with four sterigmata and a simple septum at the base, 21.5–26.7 × 5.7–7.4 μm; basidioles numerous, in shape similar to basidia but smaller. ***Basidiospores*.**

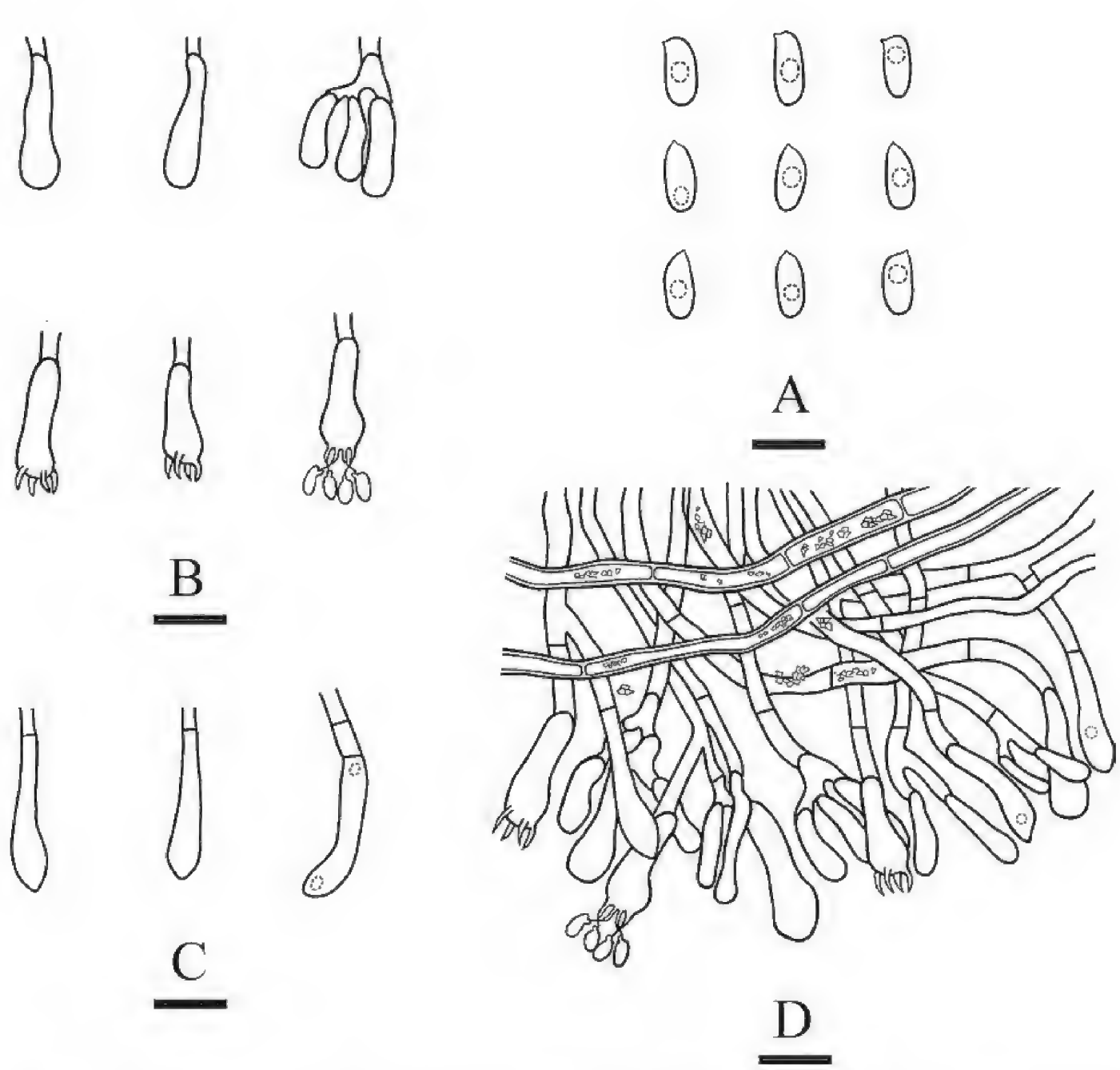

Figure 7. Microscopic structures of *Crystallicutis albomarginata* (holotype, CLZhao 31506). **A.** Basidiospores; **B.** Basidia and basidioles; **C.** Cystidia; **D.** Part of the vertical section of hymenium. Scale bars: 5 μm (**A**); 10 μm (**B–D**).

Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (3.6–)3.8–6(–7.5) × (2–)2.6–3.7(–4.3) μm, L = 5.3 μm, W = 3.3 μm, Q = 1.63 (n = 30/1).

***Efibula punctata* Z.R Gu & C.L. Zhao, sp. nov.**

MycoBank No: 858811

Figs 11–13

Diagnosis. Differs from other *Efibula* species by its membranaceous, slightly gray to pale brown basidiomata, a monomitic hyphal system with simple-septate generative hyphae, and ellipsoid basidiospores measuring 4.3–6.2 × 2.2–3.3 μm.

Holotype. China • Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 27°77'N, 104°25'E, altitude 1900 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 18 July 2023, CLZhao 30011, GenBank: ITS = PV470544, nLSU = PV474189 (SWFC).

Etymology. *Punctata* (Latin or Greek origin): refers to the species having cushion-shaped hymenial surface of the type specimens.

Description. *Basidiomata*. Annual, resupinate, closely adnate, thin membranaceous, without odor or taste when fresh, up to 10 cm long, 2 cm wide, and 200 μm thick at center. Hymenophore smooth, cream to slightly brown when fresh, slightly gray to pale brown upon drying. Sterile margin narrow, cream to slightly brown, up to 1 mm.

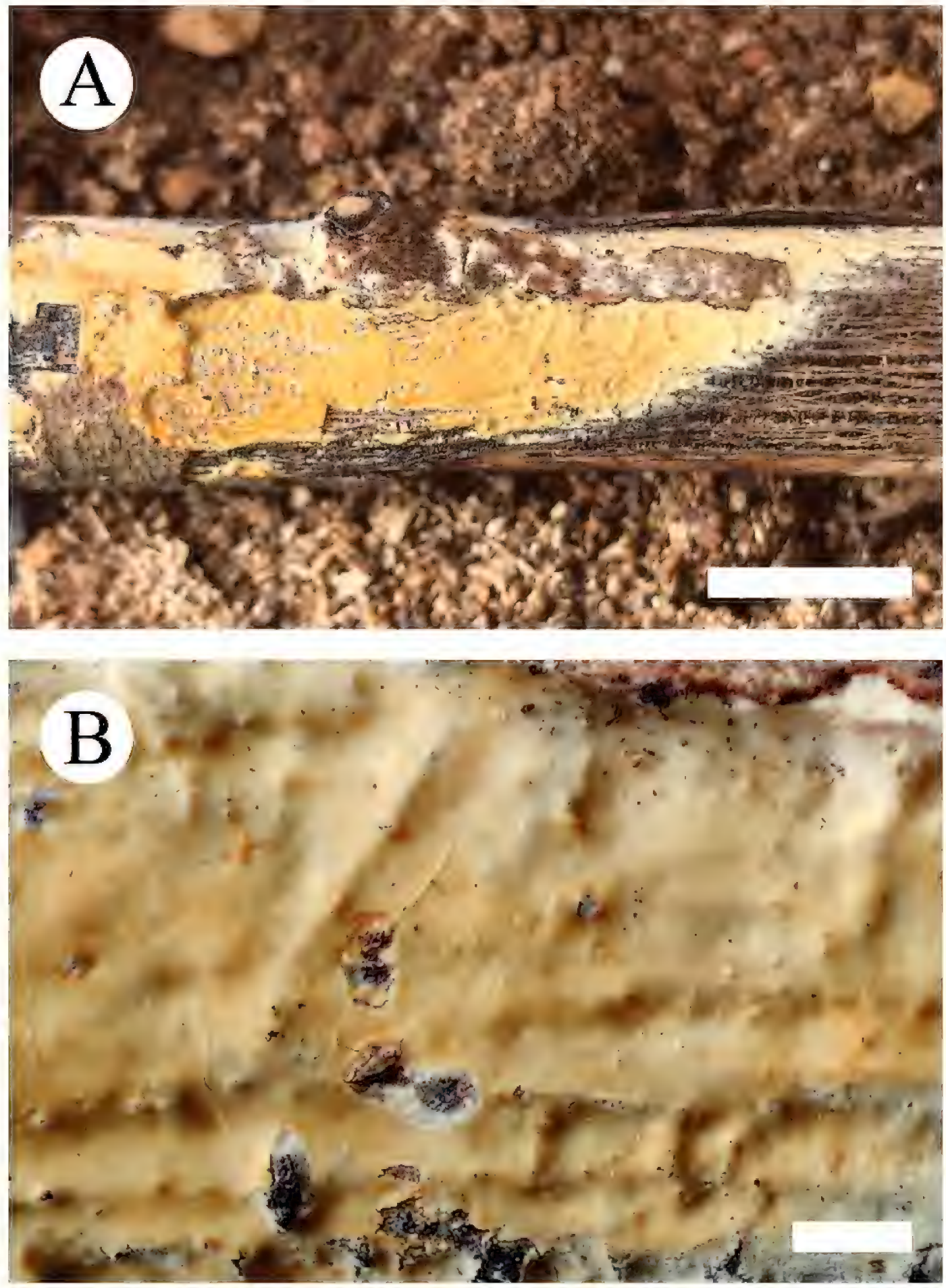

Figure 8. Basidiomata of *Efibula glossophora* (holotype, CLZhao 22744). **A.** Basidiomata on the substrate; **B.** Macroscopic characteristics of hymenophore. Scale bars: 1 cm (**A**); 1 mm (**B**).

***Hyphal system*.** Monomitic; generative hyphae with simple septa, colorless, thin-walled, smooth, branched, interwoven, 1.5–3.5 µm in diameter; IKI–, CB–; tissues unchanged in KOH. ***Hymenium*.** Cystidia absent, cystidoles mostly subfusiform, colorless, thin-walled, smooth, 9.8–22 × 2.8–5.7 µm. Basidia subcylindrical to subclavate, slightly flexuous, with a basal simple septum and four sterigmata, 11.8–19.4 × 3.7–5.9 µm; basidioles numerous, in shape similar to basidia but smaller. ***Basidiospores*.** Basidiospores ellipsoid, colorless, thin-walled, IKI–, CB–, (3.6–)4.3–6.2(–6.7) × (1.8–)2.2–3.3(–3.9) µm, L = 5.17 µm, W = 2.74 µm, Q = 1.81–1.92 (n = 240/8).

Additional specimens examined (paratypes). China • Yunnan Province, Dali, Weishan County, Leqiu Town, Zhongyao Village, GPS coordinates: 25°01'N,

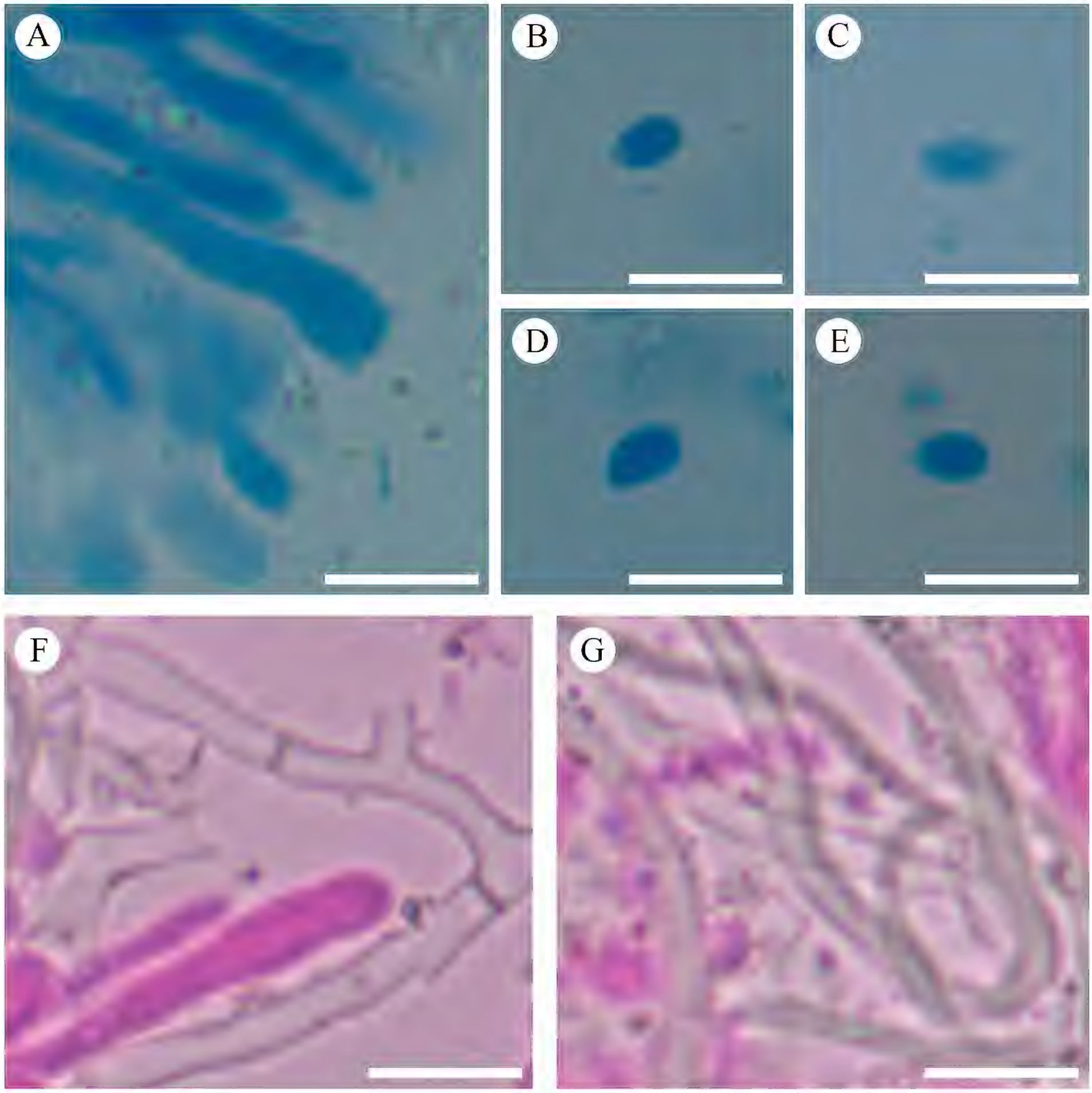

Figure 9. Sections of hymenium of *Efibula glossophora* (holotype, CLZhao 22744). **A.** Basidia and basidioles; **B–E.** Basidiospores; **F, G.** Part of the generative hyphae. Scale bars: 10 μm (**A–G**); 10 × 100 Oil.

100°4'E, altitude 1900 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 19 July 2022, CLZhao 22764, GenBank: ITS = PV470541, nLSU = PV474186 (SWFC). • Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 24°42'N, 97°56'E, altitude 850 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 17 July 2023, CLZhao 29674, GenBank: ITS = PV470542; nLSU = PV474187; CLZhao 29678, GenBank: ITS = PV470543; nLSU = PV474188; on the fallen angiosperm branch, leg. C.L. Zhao, 18 July 2023, CLZhao 30054, GenBank: ITS = PV470545; nLSU = PV474190; on the fallen angiosperm branch, leg. C.L. Zhao, 20 July 2023, CLZhao 30615, GenBank: ITS = PV470546; nLSU = PV474191, CLZhao 30637, GenBank: ITS = PV470547; nLSU = PV474192, CLZhao 30648, GenBank: ITS = PV470548; nLSU = PV474193, CLZhao 30659, GenBank: ITS = PV470549; nLSU = PV474194, CLZhao 30664,

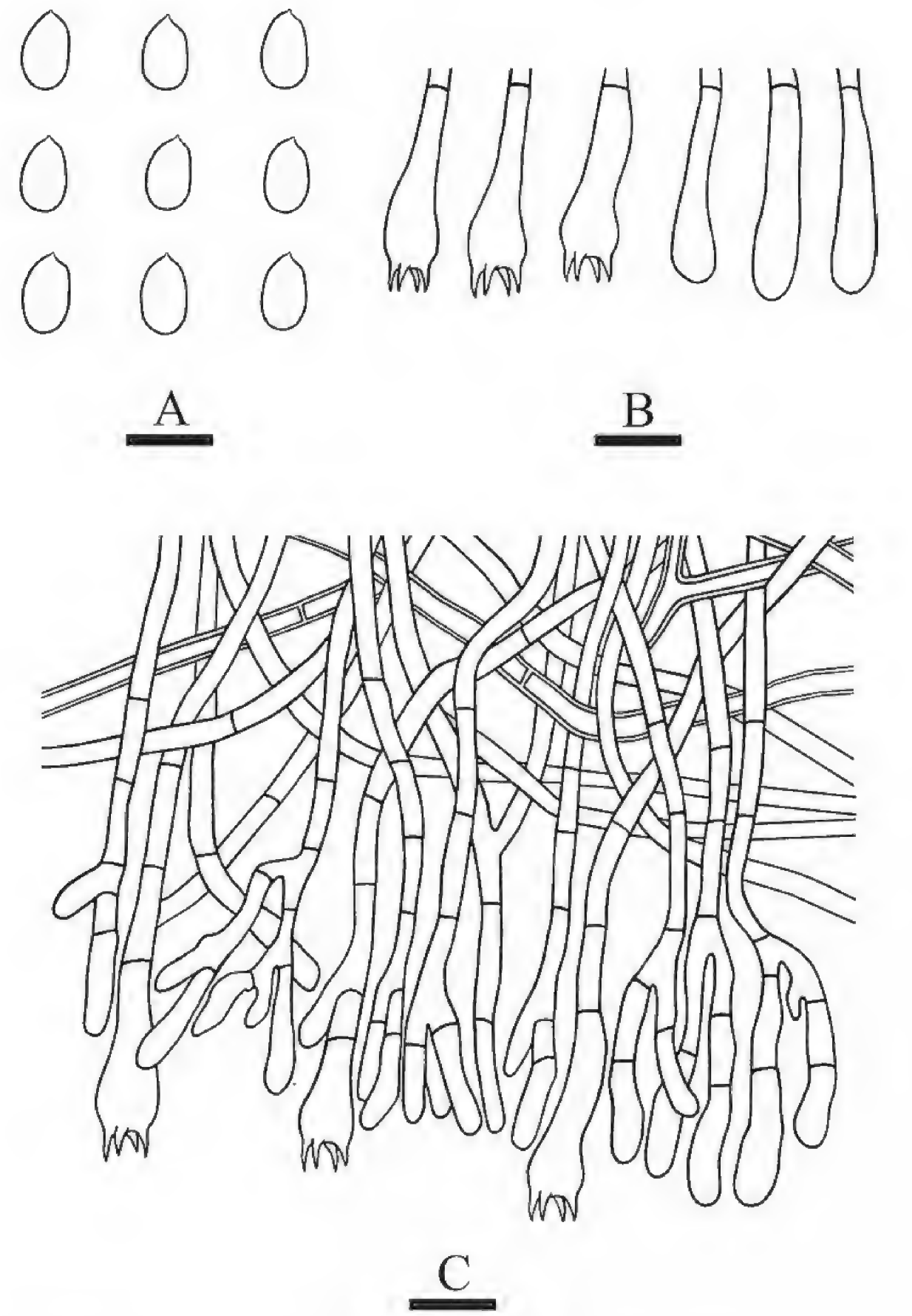

Figure 10. Microscopic structures of *Efibula glossophora* (holotype, CLZhao 22744). **A.** Basidiospores; **B.** Basidia and basidioles; **C.** Part of the vertical section of hymenium. Scale bars: 5 μm (**A**); 10 μm (**B**, **C**).

GenBank: ITS = PV470550; nLSU = PV474195, CLZhao 30691, GenBank: ITS = PV470551; nLSU = PV474196, CLZhao 30718, GenBank: ITS = PV470552; nLSU = PV474197 (SWFC).

***Scopuloides farinacea* Z.R Gu & C.L. Zhao, sp. nov.**

MycoBank No: 858812

Figs 14–16

Diagnosis. Differs from other *Scopuloides* species by its coriaceous, pale cream to buff basidiomata, a monomitic hyphal system with simple-septate generative hyphae, and ellipsoid basidiospores measuring 2.8–3.5 × 1.4–2 μm.

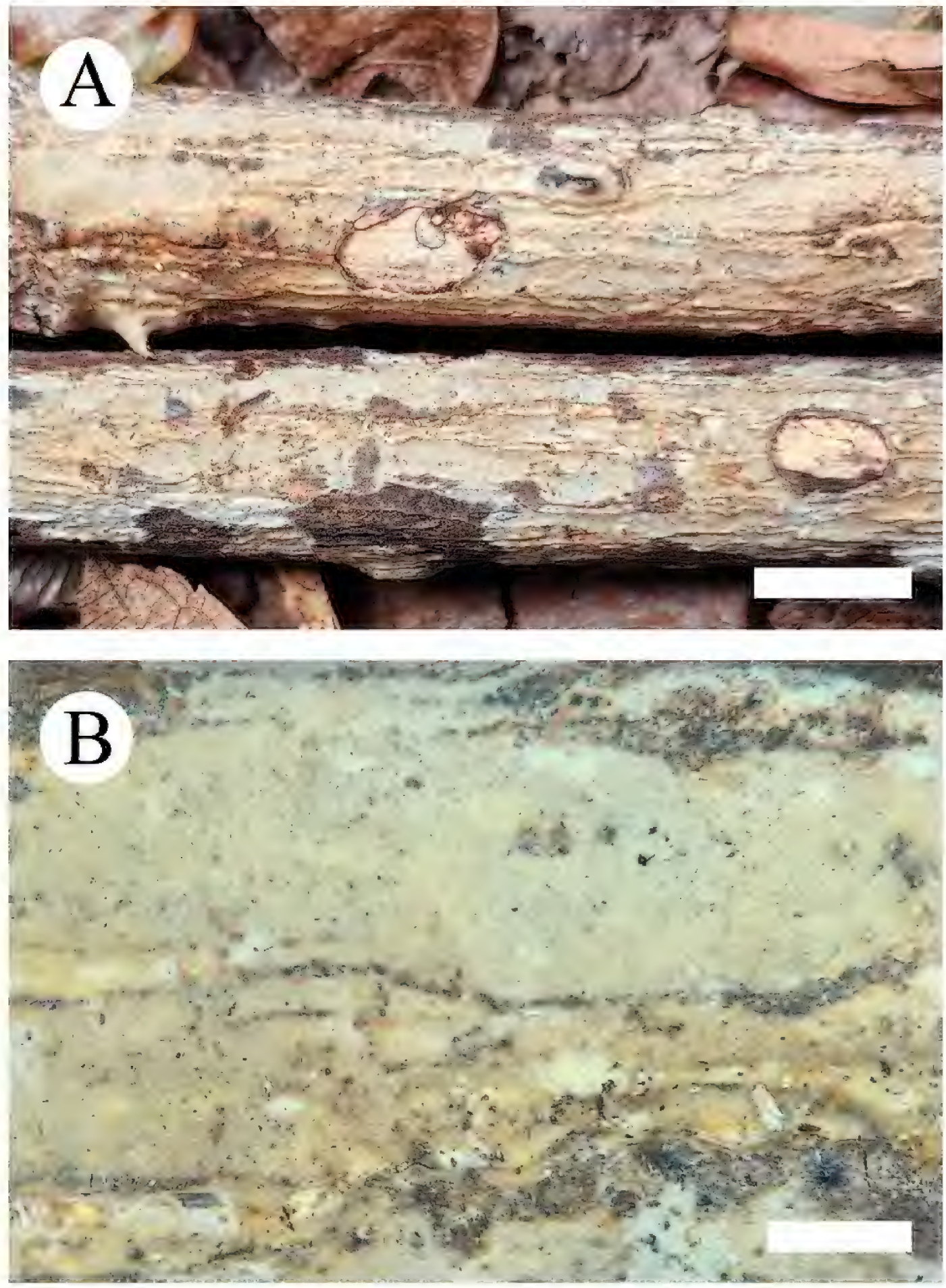

Figure 11. Basidiomata of *Efibula punctata* (holotype, CLZhao 30011). **A.** Basidiomata on the substrate; **B.** Macroscopic characteristics of hymenophore. Scale bars: 1 cm (**A**); 1 mm (**B**).

Holotype. CHINA • Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 24°42'N, 97°56'E, altitude 850 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 19 July 2023, CLZhao 30181, GenBank: ITS = PV470559; nLSU = PV474204 (SWFC).

Etymology. *Farinacea* (Latin or Greek origin): refers to the farinaceous hymenial surface of the type specimens.

Description. *Basidiomata*. Annual, resupinate, closely adnate, coriaceous, without odor or taste when fresh, up to 20 cm long, 3 cm wide, and 400 μm thick at center. Hymenophore grandinoid, white to cream when fresh, pale cream to buff upon drying. Sterile margin white to pale cream, up to 1 mm.

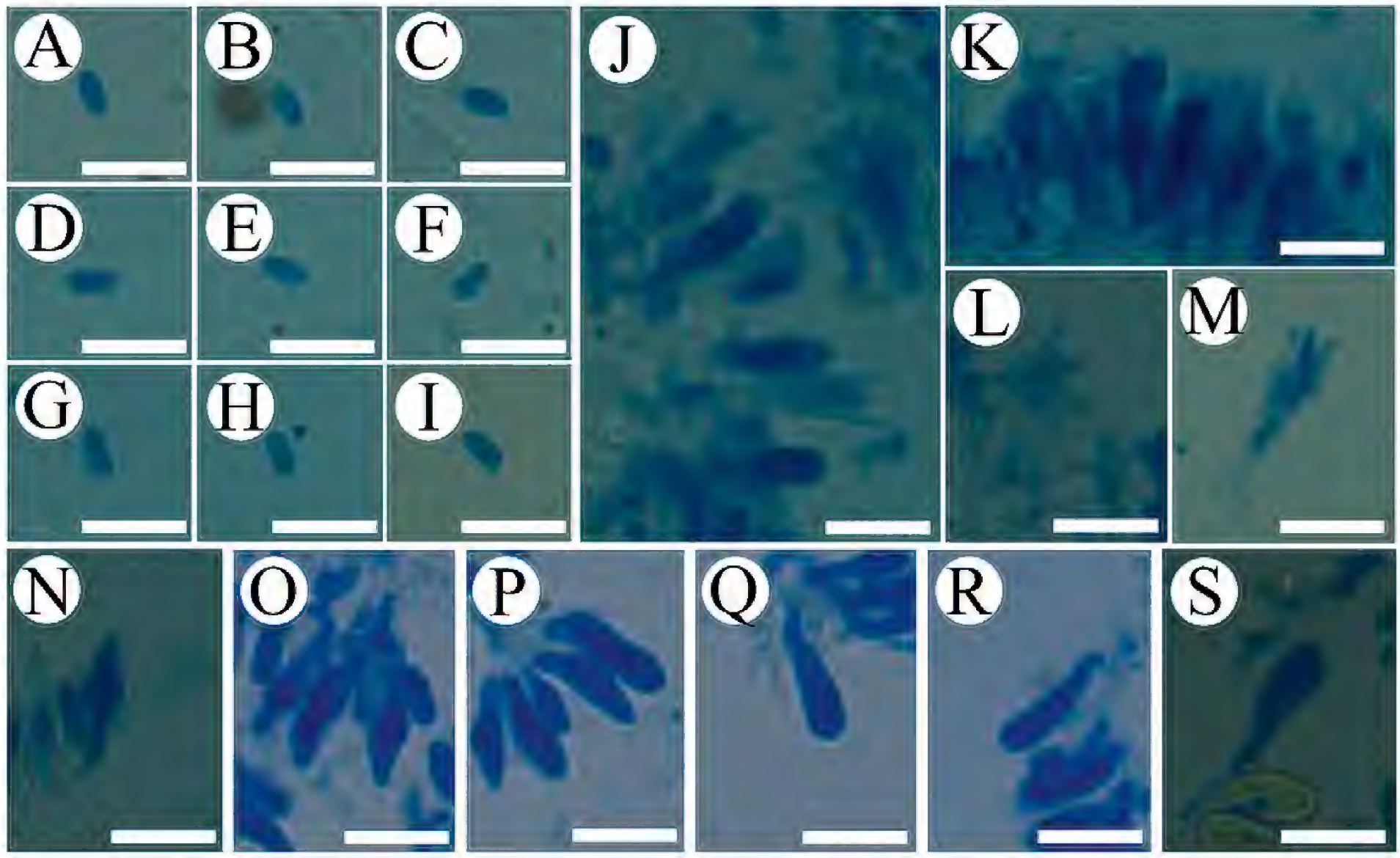

Figure 12. Sections of hymenium of *Efibula punctata* (holotype, CLZhao 30011). **A–I.** Basidiospores; **J–M.** Basidia; **N–P.** Cystidoles; **Q–S.** Basidioles. Scale bars: 10 μm (**A–S**); 10 × 100 Oil.

***Hyphal system*.** Monomitic; generative hyphae with simple septa, colorless, thin- to slightly thick-walled, smooth, branched, more or less parallel with substrate, 1.7–5.5 μm in diameter, IKI–, CB–; tissues unchanged in KOH. ***Hymenium*.** Lamprocystidia abundant, conical or subulate, colorless, simple-septate at base, heavily encrusted, originating from trama or subiculum, immersed or projecting, 21.2–39.5 × 6–13 μm. Basidia subcylindrical, slightly flexuous, with a basal simple septum and four sterigmata, 4.6–8 × 1.8–2.7 μm; basidioles numerous, in shape similar to basidia but slightly smaller. ***Basidiospores*.** Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (2.6–)2.8–3.5(–3.7) × (1.2–)1.4–2 μm, L = 3.08 μm, W = 1.65 μm, Q = 1.79–1.92 (n = 90/3).

Additional specimens examined (paratypes). China • Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, Wangfu Waterfall, GPS coordinates: 22°19'N, 103°43'E, altitude 1800 m asl., on the fallen angiosperm branch, leg. H.M. Zhou, 18 August 2024, HMZhou 153, GenBank: ITS = PV470560, nLSU = PV474205; • Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 24°42'N, 97°56'E, altitude 850 m asl., on the angiosperm trunk, leg. C.L. Zhao, 18 July 2023, CLZhao 30005, GenBank: ITS = PV470558; nLSU = PV474203 (SWFC).

Discussion

In the present study, four new species, *Crystallicutis albomarginata*, *Efibula glossophora*, *E. punctata*, and *Scopuloides farinacea*, are described based on phylogenetic analyses and morphological characteristics.

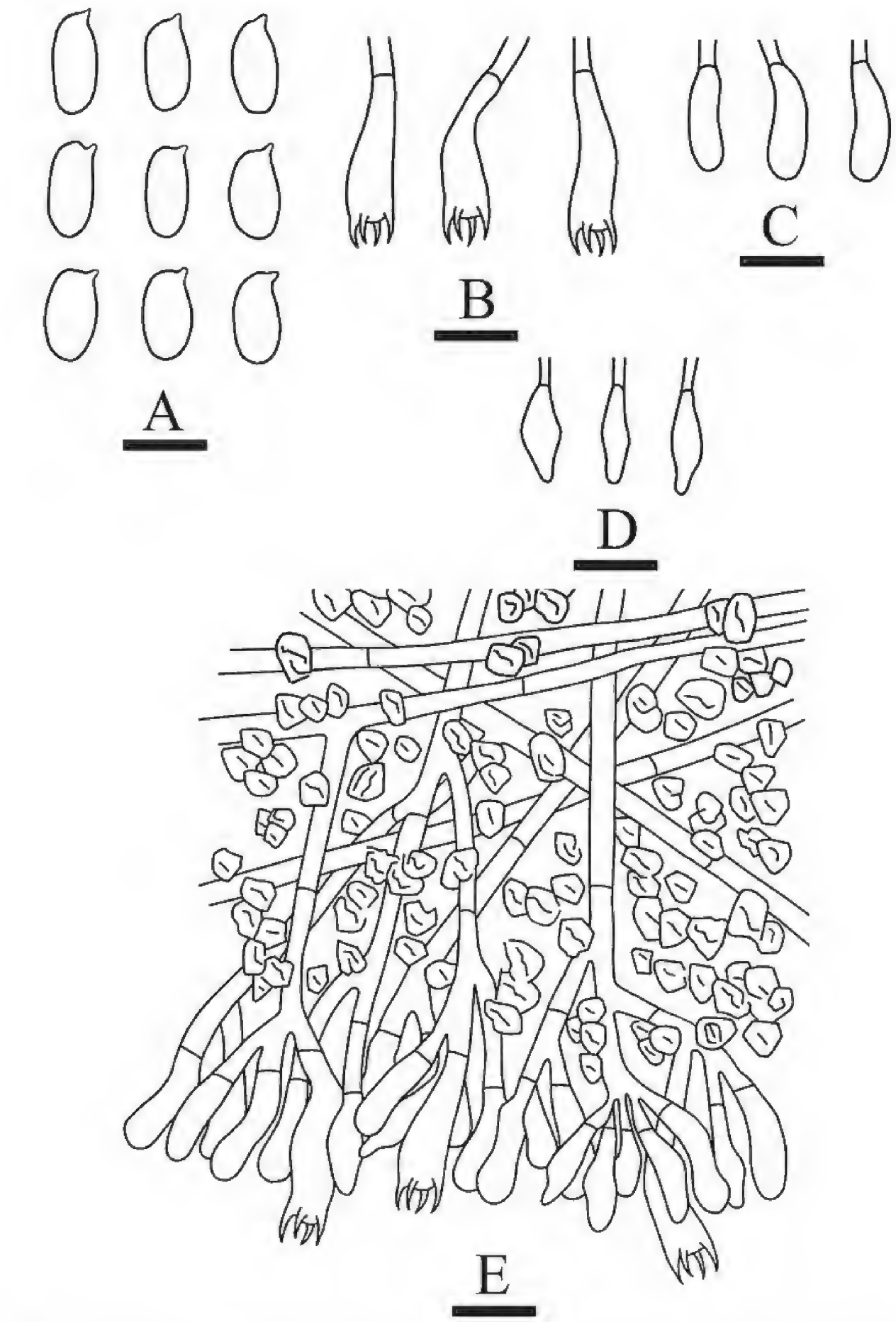

Figure 13. Microscopic structures of *Efibula punctata* (holotype, CLZhao 30011). **A.** Basidiospores; **B.** Basidia; **C.** Basidioles; **D.** Cystidoles. Scale bars: 5 µm (**A**); 10 µm (**B–D**).

Phylogenetically, three new taxa were grouped into the family Irpicaceae based on the ITS+nLSU+RPB1+RPB2+TEF1 dataset, in which *Crystallicutis albomarginata* was sister to *C. serpens* (Fig. 1). Morphologically, *C. serpens* has bigger basidia (21–32 × 4.5–5 µm; El-Gharabawy et al. 2021). *Efibula punctata* and *E. glossophora* were grouped with *E. yunnanensis* C.L. Zhao, *E. gracilis* Floudas & Hibbett, *E. hainanensis*, and *E. clarkii* Floudas & Hibbett (Fig. 1). The observed topology is strongly supported and consistent with previous findings (El-Gharabawy et al. 2021). Phylogenetic analysis based on the ITS+nLSU+RPB1+RPB2+TEF1 dataset showed that the two species were confirmed to be grouped together and clustered into the genus *Efibula*, consistent with previous research (Dong et al. 2024). *Efibula glossophora* is closely related to *E. intertexta* and *E. hainanensis* (Fig. 2); *E. punctata* was sister to *E. intertexta* (Fig. 2). Morphologically, *Efibula glossophora* is similar to *E. intertexta* and *E. hainanensis*,

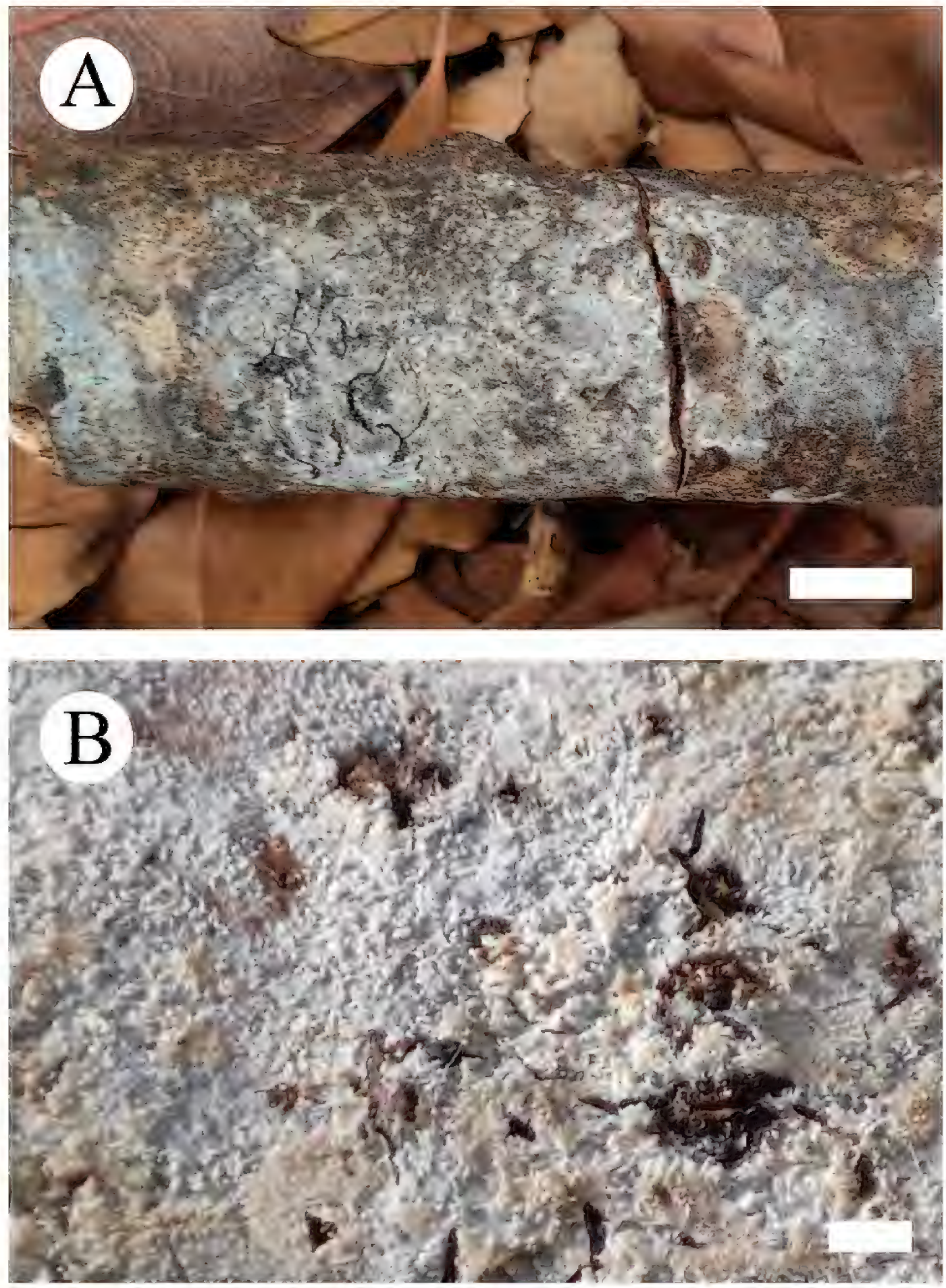

Figure 14. Basidiomata of *Scopuloides farinacea* (holotype, CLZhao 30181). **A.** Basidiomata on the substrate; **B.** Macroscopic characteristics of hymenophore. Scale bars: 1 cm (**A**); 1 mm (**B**).

but *E. intertexta* has bigger basidia (30–35 × 4.5–5 µm; Chen et al. 2021), and *E. hainanensis* has rare cystidia (Li et al. 2022). *Efibula punctata* differs from *E. intertexta* by having bigger basidia (30–35 × 4.5–5 µm; Chen et al. 2021).

The morphological distinctions among *Crystallicutis* species, including the newly described taxon *Crystallicutis albomarginata*, are delineated through the comparative analysis presented in Table 2. Comparative characteristics of *Efibula* species are tabulated in Table 3 to establish taxonomic differentiation for the newly proposed species.

Phylogenetically, four *Scopuloides* species—*S. allantoidea*, *S. dimorpha* (Sang H. Lin & Z.C. Chen) C.C. Chen & Sheng H. Wu, *S. hydnoides*, and *S. rimosa* (Cooke) Jülich—grouped together and formed a strongly supported

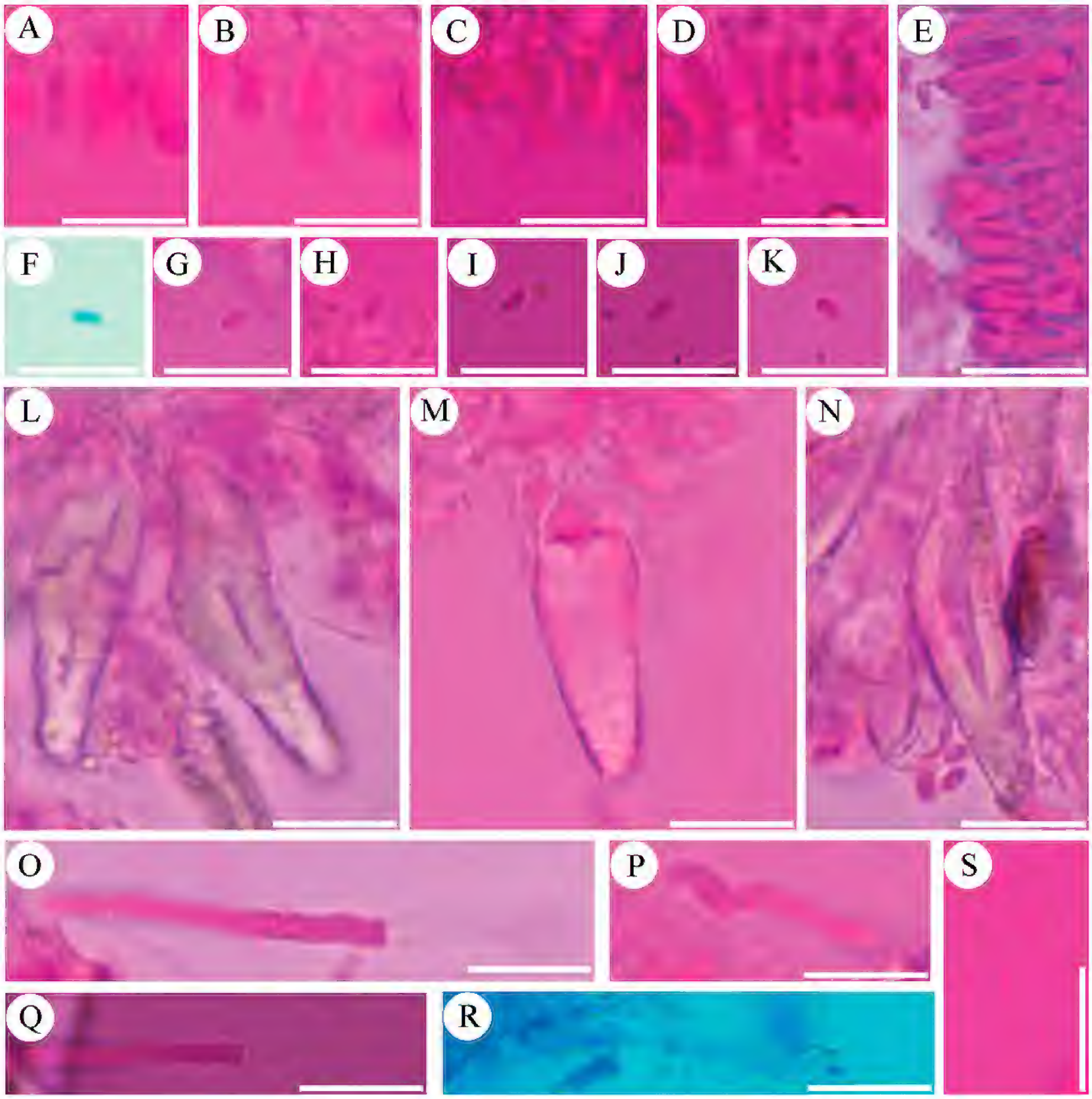

Figure 15. Sections of hymenium of *Scopuloides farinacea* (holotype, CLZhao 30181). **A–E.** Basidia and basidioles; **F–K.** Basidiospores; **L–N.** Cystidia; **O–S.** Part of the generative hyphae. Scale bars: 10 μm (**A–S**); 10 × 100 Oil.

clade based on the ITS+nLSU+TEF1+mt-SSU+GAPDH+RPB1+RPB2 sequences (Chen et al. 2021; Zhao et al. 2023). In our study, phylogenetic analysis based on ITS+nLSU+RPB1+RPB2+TEF1 data provided molecular evidence supporting *Scopuloides farinacea* as a member of Meruliaceae, in which *S. farinacea* was confirmed to group with *S. allantoidea* and *S. rimosa* (Fig. 3), consistent with previous findings (Liu et al. 2022; Zhou et al. 2024; Li et al. 2025). Based on ITS+nLSU+RPB2+TEF1 phylogenetic analysis, the new species *Scopuloides farinacea* was sister to *S. allantoidea* (Fig. 4), consistent with previous research (Gu et al. 2024). Morphologically, *Scopuloides farinacea* differs from *S. allantoidea* by having greyish, white to cream basidiomata, while the latter has larger basidia (9–12 × 3–4 μm; Chen et al. 2021). *Scopuloides farinacea* differs from *S. rimosa* by the latter having a greyish hymenial surface, larger basidia (10–12 × 3–4 μm), and larger lamprocystidia (40–50 × 8–10 μm; Jülich 1982).

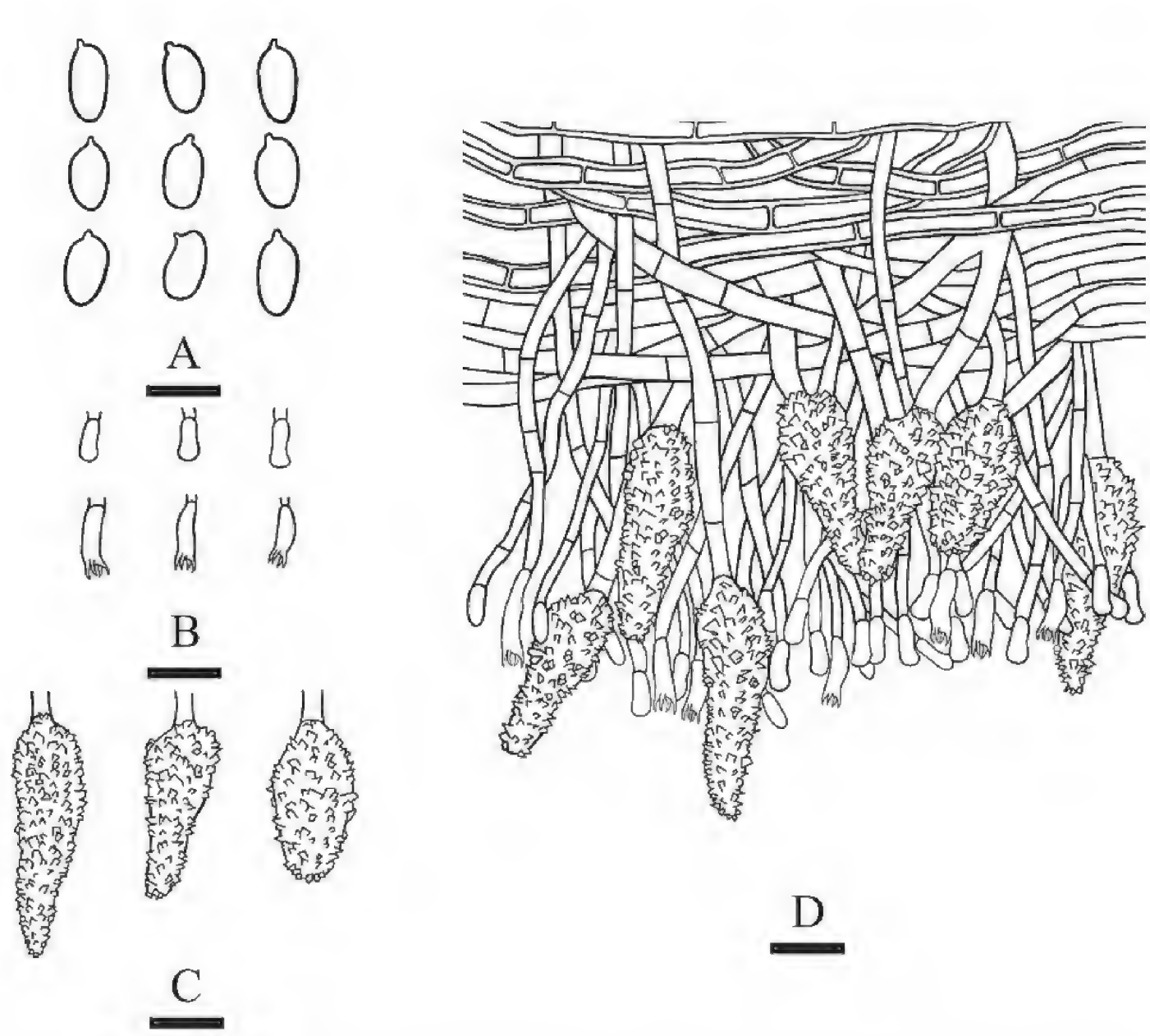

Figure 16. Microscopic structures of *Scopuloides farinacea* (holotype, CLZhao 30181). **A.** Basidiospores; **B.** Basidia and basidioles; **C.** Cystidia; **D.** Part of the vertical section of hymenium. Scale bars: 5 μm (**A**); 10 μm (**B–D**).

Table 2. A morphological comparison between *Crystallicutis albomarginata* and four similar species in the genus *Crystallicutis*.

Species name	Hymenial surface	Generative Hyphae	Cystidia	Basidia	Basidiospores	References
Crystallicutis albomarginata	**Membranaceous, smooth, slightly pink to orange**	**Monomitic, simple septa, thin to slightly thick-walled, rarely branched**	**Fusiform, thin-walled, 12.5–20 × 3.5–6 μm**	**Clavate, 12.1–19.4 × 3.8–6 μm**	**Narrowly ellipsoid, thin-walled, 1-2 guttulae, 3.7–4.4 × 1.9–2.8 μm**	**Present study**
Crystallicutis damiettensis	Ceraceous, tuberculate to papillate-warty, honey-yellow	Monomitic, clamp, frequent stumpy branches	Long, spear-shaped, thin-walled, 22–25 × 4.0–5.0 μm; Cystidioles are fusiform, 18–22 × 3.0–4.0 μm	Clavate, 12.0–15.0 × 6.0–7.5 μm	Ovoid to ellipsoid, thick-walled, 4.0–5.0 × 3.0–3.5 μm	El-Gharabawy et al. (2016)
Crystallicutis huangshanensis	Honey-yellow to olivaceous-buff	Monomitic, simple septa, thin- to slightly thick-walled, moderately branched	–	Clavate, 13.4–19.5 × 3.6–5.2 μm	Broadly ellipsoid; thin-walled, 3–3.9 × 2–2.4 μm	El-Gharabawy et al. (2021
Crystallicutis rajchenbergii	Non-ceraceous, smooth with small cracks, honey-yellow colored with tan to brownish	Monomitic, thin-walled, densely branched	Clavate with a sharp apex,thick walled, 25–30 × 4–5 μm; Cystidioles fusiform, thick-walled, 10 × 3 μm	Ovoid to clavate, 8–10 × 5–6 μm	Subellipsoid, thick-walled, 10–15 × 3–6 μm	El-Gharabawy et al. (2016)
Crystallicutis serpens	Ceraceous, smooth to slightly merulioid, hymenial surface buff, rosy buff to salmon	Monomitic, clamp, thin-walled	–	Narrowly clavate, 21–32 × 4.5–5 μm	Narrowly ellipsoid, thin-walled, 3.5–5 × 1.5–2.5 μm	Maekawa (1994)

A morphometric comparison of *Scopuloides* species reveals diagnostic features that characterize the newly recognized species *S. farinacea* (Table 4). Phylogenetic analysis also indicated that *S. yunnanensis* was nested in the genus *Scopuloides*.

Table 3. A morphological comparison between two new species and similar species in the genus *Efibula*.

Species name	Hymenial surface	Cystidia	Basidia (μm)	Basidiospores (μm)	References
E. americana	Smooth to reticulate	Absent	20–32 × 5–8	Ellipsoid to cylindrical; 5.3–6.5 × 3–3.8	Floudas and Hibbett (2015)
E. clarkii	Slightly tuberculate	Absent	25–39 × 5–7.5	Oblong to ellipsoid; 6–7 × 3–3.5	Floudas and Hibbett (2015)
E. glossophora	**Smooth**	**Absent**	**21.5–26.7 × 5.7–7.4**	**Ellipsoid; 3.8–6 × 2.6–3.7**	**Present study**
E. gracilis	Smooth	Absent	17–30 × 5–6.5	Ellipsoid to oblong; 5.5–7 × 3.3–4	Floudas and Hibbett (2015)
E. grandinosa	Grandinioid	Absent	36–43 × 5–7	Ellipsoid; 6–6.8 × 3.7–4	Li et al. (2022)
E. hainanensis	Smooth	Rare	15–26 × 4–6	Ellipsoid to broadly ellipsoid; 4.2–5.5 × 2.8–3.2	Li et al. (2022)
E. intertexta	Smooth	Absent	30–35 × 4.5–5	Cylindrical; 5.6–6.4 × 2.2–2.6	Chen et al. (2021)
E. matsuensis	Smooth	Absent	18–25 × 6.5–8	Ellipsoid to cylindrical; 7.4–8.6 × 3.8–4.4	Chen et al. (2021)
E. punctata	**Smooth**	**Absent**	**11.8–19.4 × 3.7–5.9**	**Ellipsoid; 4.3–6.2 × 2.2–3.3**	**Present study**
E. rodriguezarmasiae	Smooth to tuberculate	Absent	35–48 × 6–8	Ellipsoid; 6–7 × 4–5	Boonmee et al. (2021)
E. shenghuae	Smooth to grandinioid	Absent	23–38 × 4.5–7	Oblong ellipsoid; 6–6.5 × 3–3.5	Li et al. (2022)
E.subglobispora	Smooth	Absent	30–40 × 6.5–8	Broadly ellipsoid to subglobose; 6.4–8.1 × 4.5–5.8	Chen et al. (2021)
E. taiwanensis	Smooth	Absent	24–44 × 6–8	Broadly elliosoid to ovoid; 5.8–6.5 × 4–4.5	Li et al. (2022)
E. tropica	Smooth	Absent	20–40 × 5.5–8	Broadly elliosoid; 6.4–7.7 × 3.7–4.4	Chen et al. (2021)
E. tuberculata	Smooth to slightly tuberculate	Absent	18–35 × 5–6	Ellipsoid; 5.3–6.4 × 3.4–4.3	Chen et al. (2021)
E. turgida	Smooth	Absent	26–30 × 6.5–7	Cylindrical; 6.6–8.2 × 3.3–3.9	Chen et al. (2021)
E. yunnanensis	Mainly Smooth, sometimes slightly tuberculate	Absent	27–38 × 6–7	Broadly ellipsoid; 6.6–8 × 3.9–4.7	Chen et al. (2021)

Table 4. A morphological comparison between *Scopuloides farinacea* and ten similar species in the genus *Scopuloides*.

Species name	Hymenial surface	Generative Hyphae	Cystidia	Basidia	Basidiospores	References
Scopuloides allantoidea	Ceraceous to pruinose, odontioid, not cracked, grayish, white to cream	Thick-walled, branched	Lamprocystidia, conical or subulate, 30–70 × 7–17 μm; septate cystidia, cylindrical, apically capitate, rounded or narrow, 5–13 μm diam, thick-walled	Cylindrical to clavate, 9–12 × 3–4 μm	Allantoid, 3.3–3.7 × 1.2–1.4 μm	Chen et al. (2021)
Scopuloides dimorpha	Membranaceous, odontioid, not completely cracked, white, catridge buff, ivory buff or pale pinkish buff	Thin-walled, unbranched	Lamprocystidia, 35 × 5–17 μm; septate cystidia, cylindrical, fimbriatus apice, thin-walled	Subclavate to cylindrical, 15 × 3.5–3.8 μm	Ellipsoid, 3–3.2 × 1.2–1.8 μm	Lin and Chen (1990)
Scopuloides ellipsoidea	Ceraceous, grandinioid, yellowish white, gray, yellowish gray to orange gray	Thick-walled, rarely branched	Lamprocystidia, subconical to subfusiform, 18–30 × 4.5–11 μm	Subclavate to subcylindrical, 10–18 × 3–4 μm	Ellipsoid, 2.6–3.1 × 1.5–1.8 μm	Li et al. (2025)
Scopuloides farinacea	**Coriaceous, grandinoid, pale cream to buff**	**Thin to slightly thick-walled, branched**	**Lamprocystidia, conical or subulate, 21.2–39.5 × 6–13 μm**	**Subcylindrical, slightly flexuous, 4.6–8 × 1.8–2.7 μm**	**Ellipsoid, 2.8–3.5 × 1.4–2 μm**	**Present study**
Scopuloides grandinioides	Ceraceous, grandinioid, grayish orange	Thick-walled, rarely branched	Lamprocystidia, subulate to subfusiform, 45–55 × 7–14 μm; aculeal cystidia single, cylindrical, with several secondary septa, 52–90 × 6–12 μm, thick-walled	Subcylindrical, 10–15 × 3–4 μm	Allantoid to subcylindrical, 3–3.5 × 1.1–1.2 μm	Li et al. (2025)
Scopuloides hydnoides	Ceraceous, odontoid, distinctly cracked, whitish or grayish	Thick-walled, branched	Lamprocystidia, 40–60 × 8–12 μm; septate cystidia, cylindrical, Thick-walled	Subclavate, 12–15 × 3.5–4.5 μm	Short-allantoid, 3.5–4 × 1.8–2 μm	Hjortstam and Ryvarden (1979)

Species name	Hymenial surface	Generative Hyphae	Cystidia	Basidia	Basidiospores	References
Scopuloides leprosa	Membranaceous to subceraceous, smooth to irregular, rarely slightly grandinioid, deeply cracked; whitish to yellowish alutaceous, ochraceous	Thin to thick-walled, branched	Lamprocystidia, fusiform, 40–80 × 8–14 µm; cylindrical leptocystidia with obtuse or slightly swollen apex, 150 × 8–10 µm	Narrowly clavate, 20–30 × 4–6 µm	Ellipsoid, 4–5.5 × 2.5–3 µm	Boidin et al. (1993)
Scopuloides magnicystidiata	Cracking moderately, pale smoke gray to pale olive gray, older areas cartridge buff	Thick-walled, infrequently branched	Cylindrical with simple septa, often constricted at septa,150 × 20 µm, thin-walled	Clavate, 11–14 × 4–5.5 µm	Oblong to short-cylindric, 4–5 × 2–2.5 µm	Gilbertson and Nakasone (2003)
Scopuloides rimosa	Ceraceous, odontoid, more or less grayish	Thin to thick-walled	Lamprocystidia, conical, 40–50 × 8–10 µm	Subclavate, 10–12 × 3–4 µm	Suballantoid, 3.5–4.5 × 1.5–2 µm	Jülich (1982)
Scopuloides subgelatinosa	Ceraceous, widely hydnaceous to odontoid, cracks locally abundant, grayish brown, light brown to brown	Thick-walled, moderately branched	Pseudocystidia narrowly clavate with an obtuse apex or fusiform with an acute apex; 50–70 × 7–8 µm; encrusted cystidia, clavate to broadly fusiform with acute or rounded apices, 25–40 × 5.5–8 µm	–	Ellipsoid, 2.7–3 × 1.3–1.8 µm	Nakasone (2003)
Scopuloides yunnanensis	Membranaceous, grandinoid, white to slightly cream	Thin to thick-walled, rarely branched	Lamprocystidia conical or subulate, 15–34 × 5–12 µm; septate cystidia, cylindrical, apically capitate, rounded or narrow, 18.5–40.5 × 4.5–7.5 µm	Cylindrical, 7–14.5 × 3–5 µm	Allantoid, 2.8–3.7 × 1.4–2 µm	Gu et al. (2024)

Wood-inhabiting fungi are very rich in Yunnan Province of China, and many new taxa have been recently described from the province (Dai et al. 2021; Wang et al. 2021; Wu et al. 2022b; Wang et al. 2023, 2024; Dong et al. 2023; Mao et al. 2023; Yang et al. 2023, 2024; Yuan et al. 2023; Zhang et al. 2023, 2024, 2025; Zhou et al. 2024, 2025; Liu et al. 2025b; Yang et al. 2025a). However, there are still unknown taxa of wood-inhabiting fungi in this region, and more new species could be discovered through further investigations in different areas of Yunnan Province.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

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Author contributions

Conceptualization, CZ and SY; methodology, CZ, HZ, and ZG; software, CZ, HZ, ZG, JZ, YL, and QD; validation, CZ and ZG; formal analysis, CZ and ZG; investigation, CZ, CQZ, SY, and ZG; resources, CZ, CQZ, RY, and SY; writing—original draft preparation, CZ, ZG, CQZ, JZ, and YL; writing—review and editing, CZ, SY, and ZG; visualization, CZ, HZ, and ZG; supervision, CZ and SY; project administration, CZ; funding acquisition, CZ. All authors have read and agreed to the published version of the manuscript.

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Data availability

All of the data that support the findings of this study are available in the main text.

References

Anonymous (1969) Flora of British fungi: colour identification chart. Her Majesty's Stationery Office, London 4.

Bernicchia A, Gorjón SP (2010) Corticiaceae s.l. In: Fungi Europaei 12. Edizioni Candusso, Alassio, Italia.

Bhunjun CS, Niskanen T, Suwannarach N, Wannathes N, Chen YJ, Mckenzie E, Maharachchikumbura S, Buyck B, Zhao CL, Fan YG, Zhang JY, Dissanayake AJ, Sandamali D, Jayawardena RS, Kumla J, Padamsee M, Chen YY, Liimatainen K, Ammirati JF, Phukhamsakda C, Liu JK, Phonrob W, Randrianjohany E, Hongsanan S, Cheewangkoon R, Bundhun D, Khuna S, Yu WJ, Deng LS, Lu YZ, Hyde KD, Lumyong S (2022) The numbers of fungi: Are the most speciose genera truly diverse? Fungal Diversity 114(1): 387–462. https://doi.org/10.1007/s13225-022-00501-4

Binder M, Hibbett DS, Larsson KH, Larsson E, Langer E, Langer G (2005) The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (Homobasidiomycetes). Systematics and Biodiversity 3: 113–157. https://doi.org/10.1017/S1477200005001623

Boidin J, Lanquetin P, Gilles G (1993) Contribution à la connaissance des Phanerochaetoideae de France (Basidiomycotina). Cryptogamie. Mycologie 14(3): 195–206. https://doi.org/10.5962/p.354381

Boonmee S, Wanasinghe DN, Calabon MS, Huanraluek N, Chandrasiri SKU, Jones GEB, Rossi W, Leonardi M, Singh SK, Rana S, Singh PN, Maurya DK, Lagashetti AC, Choudhary D, Dai YC, Zhao CL, Mu YH, Yuan HS, He SH, Phookamsak R, Jiang HB, Martín MP, Dueñas M, Telleria MT, Kałucka IL, Jagodziński AM, Liimatainen K, Pereira DS, Phillips AJL, Suwannarach N, Kumla J, Khuna S, Lumyong S, Potter TB, Shivas RG, Sparks AH, Vaghefi N, Abdel-Wahab MA, Abdel-Aziz FA, Li GJ, Lin WF, Singh U, Bhatt RP, Lee HB, Nguyen TTT, Kirk PM, Dutta AK, Acharya K, Sarma VV, Niranjan M, Rajeshkumar KC, Ashtekar N, Lad S, Wijayawardene NN, Bhat DJ, Xu RJ, Wijesinghe SN, Shen HW, Luo ZL, Zhang

JY, Sysouphanthong P, Thongklang N, Bao DF, Aluthmuhandiram JVS, Abdollahzadeh J, Javadi A, Dovana F, Usman M, Khalid AN, Dissanayake AJ, Telagathoti A, Probst M, Peintner U, Garrido-Benavent I, Bóna L, Merényi Z, Boros L, Zoltán B, Stielow JB, Jiang N, Tian CM, Shams E, Dehghanizadeh F, Pordel A, Javan-Nikkhah M, Denchev TT, Denchev CM, Kemler M, Begerow D, Deng CY, Harrower E, Bozorov T, Kholmuradova T, Gafforov Y, Abdurazakov A, Xu JC, Mortimer PE, Ren GC, Jeewon R, Maharachchikumbura SSN, Phukhamsakda C, Mapook A, Hyde KD (2021) Fungal diversity notes 1387–1511: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 111: 1–335. https://doi.org/10.1007/s13225-021-00489-3

Cai J, Zou L, Wu X, Zhao CL (2023) *Physisporinus yunnanensis* sp. nov. (Polyporales, Basidiomycota) from Southern China. Phytotaxa 579(2): 098–106. http://doi.org/10.11646/phytotaxa.579.2.3

Chen JJ, Cui BK (2014) *Phlebiporia bubalina* gen. et. sp. nov. (Meruliaceae, Polyporales) from Southwest China with a preliminary phylogeny based on rDNA sequences. Mycological Progress 13: 563–573. https://doi.org/10.1007/s11557-013-0940-4

Chen CC, Chen CY, Lim YW, Wu SH (2020) Phylogeny and taxonomy of *Ceriporia* and other related taxa and description of three new species. Mycologia 112: 64–82. https://doi.org/10.1080/00275514.2019.1664097

Chen CC, Chen CY, Wu SH (2021) Species diversity, taxonomy and multi-gene phylogeny of phlebioid clade (Phanerochaetaceae, Irpicaceae, Meruliaceae) of Polyporales. Fungal Diversity 111(1): 337–442. https://doi.org/10.1007/s13225-021-00490-w

Cui BK, Li HJ, Ji X, Zhou JL, Song J, Si J, Yang ZL, Dai YC (2019) Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. Fungal Diversity 97: 137–392. https://doi.org/10.1007/s13225-019-00427-4

Dai YC (2010) Hymenochaetaceae (Basidiomycota) in China. Fungal Diversity 45: 131–343. https://doi.org/10.1007/s13225-010-0066-9

Dai YC (2012) Pathogenic wood-decaying fungi on woody plants in China. Mycosystema 31: 493–509. https://doi.org/10.13346/j.mycosystema.2012.04.014

Dai YC, Zhuang JY (2010) Numbers of fungal species hitherto known in China. Mycosystema 29: 625–628. https://doi.org/10.13346/j.mycosystema.2010.05.003

Dai YC, Yang ZL, Cui BK, Wu G, Yuan HS, Zhou LW, He SH, Ge ZW, Wu F, Wei YL, Yuan Y, Si J (2021) Diversity and systematics of the important macrofungi in Chinese forests. Mycosystema 40: 770–805. https://doi.org/10.13346/j.mycosystema.210036

Dong JH, Gu JY, Zhao CL (2023) Diversity of wood-decaying fungi in Wenshan Area, Yunnan Province, China. Mycosystema 42: 638–662. https://doi.org/10.13346/j.mycosystema.220205

Dong JH, Li Q, Yuan Q, Luo YX, Zhang XC, Dai YF, Zhou Q, Liu XF, Deng YL, Zhou HM, Muhammad A, Zhao CL (2024) Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. Mycosphere 15(1): 1110–1293. https://doi.org/10.5943/mycosphere/15/1/10

Dvoˇrák D, Bˇet'ák J, Tomšovský M (2014) *Aurantiporus alborubescens* (Basidiomycota, Polyporales) first record in the Carpathians and notes on its systematic position. Czech Mycology 66: 71–84. https://doi.org/10.33585/cmy.66105

El-Gharabawy HM, Detheridge AP, El-Fallal AA, El-Sayed AKA, Griffith GW (2016) Analysis of wood decay and ligninolysis in Polyporales from the Nile Delta region of Egypt. Mycosphere 7(4): 3928–404. https://doi.org/10.5943/mycosphere/7/4/1

El-Gharabawy HM, Leal-Dutra CA, Griffith GW (2021) *Crystallicutis* gen. nov. (Irpicaceae, Basidiomycota), including *C. damiettensis* sp. nov., found on *Phoenix dactylifera* (date

palm) trunks in the Nile Delta of Egypt. Fungal Biology 125: 447–458. https://doi.org/10.1016/j.funbio.2021.01.004

Floudas D, Hibbett DS (2015) Revisiting the taxonomy of *Phanerochaete* (Polyporales, Basidiomycota) using a four gene dataset and extensive ITS sampling. Fungal Biology 119: 679–719. https://doi.org/10.1016/j.funbio.2015.04.003

Ghobad-Nejhad M, Hallenberg N (2012) Multiple evidence for recognition of *Phlebia tuberculata*, a more widespread segregate of *Phlebia livida* (Polyporales, Basidiomycota). Mycological Progress 11(1): 27–35. https://doi.org/10.1007/s11557-010-0722-1

Gilbertson RL, Nakasone KK (2003) New taxa of Hawaiian corticioid fungi are described with keys to *Crustoderma*, *Radulomyces*, and *Scopuloides*. Mycologia 95(3): 467–473. https://doi.org/10.2307/3761888

Ginns J, Lindner DL, Baronia TJ, Ryvarden L (2010) *Aurantiopileus mayanensis* a new genus and species of polypore (Polyporales, Basidiomycota) from Belize with connections to existing Asian species. North American Fungi 5: 1–10. https://doi.org/10.2509/naf2010.005.004

Girometta CE, Bernicchia A Desiderio Anthea, Savino E (2025) First record of *Phlebia tremelloidea* (Bres.) Parmasto in Italy. Italian Journal of Mycology 54: 12–18. http://doi.org/10.6092/issn.2531-7342/19437

Gómez-Montoya N, Drechsler-Santos ER, Lopes VF, Tomšovský M, Urcelay C, Robledo GL (2017) New insights on *Trametopsis* Tomšovský (Polyporales Gäum) based on phylogenetic evidences and morphological analyses of neotropical species. Phytotaxa 311: 155–167. https://doi.org/10.11646/phytotaxa.311.2.3

Gu ZR, Zhou HM, Zhao CL (2024) Morphological characteristics and phylogenetic analyses reveal *Scopuloides yunnanensis* (Polyporales, Basidiomycota), a new wood-decaying fungus from China. Phytotaxa 665(2): 85–95. https://doi.org/10.11646/phytotaxa.665.2.1

Guan QX, Zhao CL (2021) Two new corticioid species, *Hyphoderma sinense* and *H. floccosum* (Hyphodermataceae, Polyporales), from southern China. Mycosystema 40: 447–461. https://doi.org/10.13346/j.mycosystema.200382

Guindon S, Gascuel O (2003) A simple, fast and accurate algorithm to estimate large phylogenies by maximum likelihood. Systematic Biology 52(5): 696–704. https://doi.org/10.1080/10635150390235520

Hall TA (1999) Bioedit: A user-friendly biological sequence alignment editor and analysis program for windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98. https://doi.org/10.1021/bk-1999-0734.ch008

He MQ, Cao B, Liu F, Boekhout T, Denchev TT, Schoutteten N, Denchev CM, Kemler M, Gorjón SP, Begerow D, Valenzuela R, Davoodian N, Niskanen T, Vizzini A, Redhead SA, Ramírez-Cruz V, Papp V, Dudka VA, Dutta AK, García-Sandoval R, Liu XZ, Kijpornyongpan T, Savchenko A, Tedersoo L, Theelen B, Trierveiler-Pereira L, Wu F, Zamora JC, Zeng XY, Zhou LW, Liu SL, Ghobad-Nejhad M, Giachini AJ, Li GJ, Kakishima M, Olariaga I, Haelewaters D, Sulistyo B, Sugiyama J, Svantesson S, Yurkov A, Alvarado P, Antonín V, da Silva AF, Druzhinina I, Gibertoni TB, Guzmán-Dávalos L, Justo A, Karunarathna SC, Galappaththi MCA, Toome-Heller M, Hosoya T, Liimatainen K, Márquez R, Mešić A, Moncalvo JM, Nagy LG, Varga T, Orihara T, Raymundo T, Salcedo I, Silva-Filho AGS, Tkalčec Z, Wartchow F, Zhao CL, Bau T, Cabarroi-Hernández1 M, Cortés-Pérez A, Decock C, Lange RD, Weiss M, Menolli Jr N, Nilsson RH, Fan YG, Verbeken A, Gaforov Y, Meiras-Ottoni A, Mendes-Alvarenga RL, Zeng NK, Wu Q, Hyde KD, Kirk PM, Zhao RL

(2024) Phylogenomics, divergence times and notes of orders in Basidiomycota. Fungal Diversity 99: 105–367. https://doi.org/10.1007/s13225-024-00535-w

Hjortstam K, Ryvarden L (1979) Notes on Corticiaceae. IV. Mycotaxon 9: 505–519.

Huang RX, Luo KY, Zhao CL (2020) *Phlebia nigrodontea* sp. nov. in Meruliaceae (Polyporales) with a black hymenial surface. Phytotaxa 458: 195–206. https://doi.org/10.11646/phytotaxa.458.3.2

Hyde KD, Xu JC, Rapior S, Jeewon R, Lumyong S, Niego AGT, Abeywickrama PD, Aluthmuhandiram JVS, Brahmanage RS, Brooks S, Chaiyasen A, Chethana KWT, Chomnunti P, Chepkirui C, Chuankid B, de Silva NI, Doilom M, Faulds C, Gentekaki E, Gopalan V, Kakumyan P, Harishchandra D, Hemachandran H, Hongsanan S, Karunarathna A, Karunarathna SC, Khan S, Kumla J, Jayawardena RS, Liu JK, Liu N, Luangharn T, Macabeo APG, Marasinghe DS, Meeks D, Mortimer PE, Mueller P, Nadir S, Nataraja KN, Nontachaiyapoom S, O'Brien M, Penkhrue W, Phukhamsakda C, Ramanan US, Rathnayaka AR, Sadaba RB, Sandargo B, Samarakoon BC, Tennakoon DS, Siva R, Sriprom W, Suryanarayanan TS, Sujarit K, Suwannarach N, Suwunwong T, Thongbai B, Thongklang N, Deping W, Wijesinghe SN, Winiski J, Yan J, Yasanthika E, Stadler M (2019) The amazing potential of fungi: 50 ways we can exploit fungi industrially. Fungal Diversity 97: 1–136. https://doi.org/10.1007/s13225-019-00430-9

Hyde KD, Noorabadi MT, Thiyagaraja V, He MQ, Johnston PR, Wijesinghe SN, Armand A, Biketova AY, Chethana KWT, Erdoğdu M, Ge ZW, Groenewald JZ, Hongsanan S, Kušan I, Leontyev DV, Li DW, Lin CG, Liu NG, Maharachchikumbura SSN, Matočec N, May TW, McKenzie EHC, Mešić A, Perera RH, Phukhamsakda C, Piątek M, Samarakoon MC, Selcuk F, Senanayake IC, Tanney JB, Tian Q, Vizzini A, Wanasinghe DN, Wannasawang N, Wijayawardene NN, Zhao RL, Abdel-Wahab MA, Abdollahzadeh J, Abeywickrama PD, Abhinav, Absalan S, Acharya K, Afshari N, Afshan NS, Afzalinia S, Ahmadpour SA, Akulov O, Alizadeh A, Alizadeh M, Al-Sadi AM, Alves A, Alves VCS, Alves-Silva G, Antonín V, Aouali S, Aptroot A, Apurillo CCS, Arias RM, Asgari, B, Asghari R, Assis DMA, Assyov B, Atienza V, Aumentado HDR, Avasthi S, Azevedo E, Bakhshi M, Bao DF, Baral HO, Barata M, Barbosa KD, Barbosa RN, Barbosa FR, Baroncelli R, Barreto GG, Baschien C, Bennett RM, Bera I, Bezerra JDP, Bhunjun CS, Bianchinotti MV, Błaszkowski J, Boekhout T, Bonito GM, Boonmee S, Boonyuen N, Bortnikov FM, Bregant C, Bundhun D, Burgaud G, Buyck B, Caeiro MF, Cabarroi-Hernández M, Cai M Feng, Cai L, Calabon MS, Calaça FJS, Callalli M, Câmara MPS, Cano-Lira J, Cao B, Carlavilla JR, Carvalho A, Carvalho TG, Castañeda-Ruiz RF, Catania MDV, Cazabonne J, Cedeño-Sanchez M, Chaharmiri-Dokhaharani S, Chaiwan N, Chakraborty N, Cheewankoon R, Chen C, Chen J, Chen Q, Chen YP, Chinaglia S, Coelho-Nascimento CC, Coleine C, CostaRezende DH, Cortés-Pérez A, Crouch, JA, Crous PW, Cruz RHSF, Czachura P, Damm U, Darmostuk V, Daroodi Z, Das K, Das K, Davoodian N, Davydov EA, da Silva GA, da Silva IR, da Silva RMF, da Silva Santos AC, Dai DQ, Dai YC, de Groot Michiel D, De Kesel A, De Lange R, de Medeiros EV, de Souza CFA, de Souza FA, dela Cruz TEE, Decock C, Delgado G, Denchev CM, Denchev TT, Deng YL, Dentinger BTM, Devadatha B, Dianese JC, Dima B, Doilom M, Dissanayake AJ, Dissanayake DMLS, Dissanayake LS, Diniz AG, Dolatabadi S, Dong JH, Dong W, Dong ZY, Drechsler-Santos ER, Druzhinina IS, Du TY, Dubey MK, Dutta AK, Elliott TF, Elshahed MS, Egidi E, Eisvand P, Fan L, Fan X, Fan XL, Fedosova AG, Ferro LO, Fiuza PO, Flakus A, W. Fonseca EO, Fryar SC, Gabaldón T, Gajanayake AJ, Gannibal PB, Gao F, GarcíaSánchez D, García-Sandoval R, Garrido-Benavent I, Garzoli L, Gasca-Pineda J, Gautam AK, Gené J, Ghobad-Nejhad M, Ghosh A, Giachini AJ, Gibertoni TB, Gentekaki E, Gmoshinskiy VI, GóesNeto A, Gomdola D, Gorjón SP, Goto BT, Granados-Montero MM, Griffith GW,

Groenewald M, Grossart H-P, Gu ZR, Gueidan C, Gunarathne A, Gunaseelan S, Guo SL, Gusmão LFP, Gutierrez AC, Guzmán-Dávalos L, Haelewaters D, Haituk H, Halling RE, He SC, Heredia G, HernándezRestrepo M, Hosoya T, Hoog SD, Horak E, Hou CL, Houbraken J, Htet ZH, Huang SK, Huang WJ, Hurdeal VG, Hustad VP, Inácio CA, Janik P, Jayalal RGU, Jayasiri SC, Jayawardena RS, Jeewon R, Jerônimo GH, Jin J, Jones EBG, Joshi Y, Jurjević Ž, Justo A, Kakishima M, Kaliyaperumal M, Kang GP, Kang JC, Karimi O, Karunarathna SC, Karpov SA, Kezo K, Khalid AN, Khan MK, Khuna S, Khyaju S, Kirchmair M, Klawonn I, Kraisitudomsook N, Kukwa M, Kularathnage ND, Kumar S, Lachance MA, Lado C, Latha KPD, Lee HB, Leonardi M, Lestari AS, Li C, Li H, Li J, Li Q, Li Y, Li YC, Li YX, Liao CF, Lima JLR, Lima JMS, Lima NB, Lin L, Linaldeddu BT, Linn MM, Liu F, Liu JK, Liu JW, Liu S, Liu SL, Liu XF, Liu XY, Longcore JE, Luangharn T, Luangsa-ard JJ, Lu L, Lu YZ, Lumbsch HT, Luo L, Luo M, Luo ZL, Ma J, Madagamma-na AD, Madhushan A, Madrid H, Magurno F, Magyar D, Mahadevakumar S, Malosso E, Malysh JM, Mamarabadi M, Manawasinghe IS, Manfrino RG, Manimohan P, Mao N, Mapook A, Marchese P, Marasinghe DS, Mardones M, Marin-Felix Y, Masigol H, Mehrabi M, MehrabiKoushki M, Meiras-Ottoni A de, Melo RFR, Mendes-Alvarenga RL, Mendieta S, Meng QF, Menkis A, Menolli Jr N, Mikšík M, Miller SL, Moncada B, Moncalvo JM, Monteiro JS, Monteiro M, Mora-Montes HM, Moroz EL, Moura JC, Mu-hammad U, Mukhopadhyay S, Nagy GL, Najam ul Sehar A, Najafiniya M, Nanayakkara CM, Naseer A, Nascimento ECR, Nascimento SS, Neuhauser S, Neves MA, Niazi AR, Nie Yong, Nilsson RH, Nogueira PTS, Novozhilov YK, Noordeloos M, Norphanphoun C, Nuñez Otaño N, O'Donnell RP, Oehl F, Oliveira JA, Oliveira Junior I, Oliveira NVL, Oliveira PHF, Orihara T, Oset M, Pang KL, Papp V, Pathirana LS, Peintner U, Pem D, Pereira OL, Pérez-Moreno J, Pérez-Ortega S, Péter G, Pires-Zottarelli CLA, Phonema-ny M, Phongeun S, Pošta A, Prazeres JFSA, Quan Y, Quandt CA, Queiroz MB, Radek R, Rahnama K, Raj KNA, Rajeshkumar KC, Rajwar Soumyadeep, Ralaiveloarisoa AB, Rämä T, Ramírez-Cruz V, Rambold G, Rathnayaka AR, Raza M, Ren GC, Rinaldi AC, Rivas-Ferreiro M, Robledo GL, Ronikier A, Rossi W, Rusevska K, Ryberg M, Safi A, Salimi F, Salvador-Montoya CA, Samant B, Samaradiwakara NP, Sánchez-Castro I, Sandoval-Denis M, Santiago ALCMA, Santos ACDS, Santos LA dos, Sarma VV, Sarwar S. Savchenko A, Savchenko K, Saxena RK, Schoutteten N, Selbmann L, Ševčíková H, Sharma A, Shen HW, Shen YM, Shu YX, Silva HF, Silva-Filho AGS, Silva VSH, Simmons DR, Singh R, Sir EB, Sohrabi M, Souza FA, Souza-Motta CM, Sriindrasutdhi V, Sruthi OP, Stadler M, Stemler J, Stephenson SL, Stoyneva-Gaertner MP, Strassert JFH, Stry-jak-Bogacka M, Su H, Sun YR, Svantesson S, Sysouphanthong P, Takamatsu S, Tan TH, Tanaka K, Tang C, Tang X, Taylor JE, Taylor PWJ, Tennakoon DS, Thakshila SAD, Thambugala KM, Thamodini GK, Thilanga D, Thines M, Tiago PV, Tian XG, Tian WH, Tibpromma S, Tkalčec Z, Tokarev YS, Tomšovský M, Torruella G, Tsurykau A, Udayan-ga D, Ulukapı M, Untereiner WA, Usman M, Uzunov BA, Vadthanarat S, Valenzuela R, Van den Wyngaert S, Van Vooren N, Velez P, Verma RK, Vieira LC Vieira WAS, Vinzelj JM, Tang AMC, Walker A, Walker AK,Wang QM, Wang Y, Wang XY, Wang ZY, Wan-nathes N, Wartchow F, Weerakoon G, Wei DP, Wei X, White JF, Wijesundara DSA, Wis-itrassameewong K, Worobiec G, Wu HX, Wu N, Xiong YR, Xu B, Xu JP, Xu R, Xu RF, Xu RJ, Yadav S, Yakovchenko LS, Yang HD, Yang X, Yang YH, Yang Y, Yang YY, Yoshioka R, Youssef Noha H, Yu FM, Yu ZF, Yuan LL, Yuan Q, Zabin DA, Zamora JC, Zapata CV, Zare R, Zeng M, Zeng XY, Zhang JF, Zhang JY, Zhang S, Zhang XC, Zhao CL, Zhao H, Zhao Q, Zhao H, Zhao HJ, Zhou HM, Zhu XY, Zmitrovich IV, Zucconi L, Zvyagina E (2024) The 2024 Outline of fungi and fungus-like taxa. Mycosphere 15: 5146–6239. https://doi.org/10.5943/mycosphere/15/1/25

Jülich W (1982) Notes on some Basidiomycetes (Aphyllophorales and Heterobasidiomycetes). Persoonia 11(4): 421–428.

Justo A, Hibbett DS (2011) Phylogenetic classification of *Trametes* (Basidiomycota, Polyporales) based on a five-marker dataset. Taxon 60: 1567–1583. https://doi.org/10.1002/tax.606003

Justo A, Miettinen O, Floudas D, Ortiz-Santana B, Sjokvist E, Lindner D, Nakasone K, Niemel T, Larsson KH, Ryvarden L, Hibbett D (2017) A revised family-level classification of the Polyporales (Basidiomycota). Fungal Biology 121: 798–824. https://doi.org/10.1016/j.funbio.2017.05.010

Kondratyuk TO, Kondratyuk SY, Morgaienko OO, Khimich MV, Beregova1 TV, Ostapchen LI (2015) *Pseudonadsoniella brunnea* (Meripilaceae, Agaricomycotina), a new brown yeast-like fungus producing melanin from the Antarctic; with notes on nomenclature and type confusion of *Nadsoniella nigra*. Acta Botanica Hungarica 57(3–4): 291–320. https://doi.org/10.1556/034.57.2015.3-4.5

Kuuskeri J, Mäkelä MR, Isotalo J, Oksanen I, Lundell T (2015) Lignocellulose-converting enzyme activity profiles correlate with molecular systematics and phylogeny grouping in the incoherent genus *Phlebia* (Polyporales, Basidiomycota). BMC Microbiology 15: 217. https://doi.org/10.1186/s12866-015-0538-x

Larsson KH, Spirin V, Ryvarden L, Larsson E (2025) Reclassification of eleven corticioid basidiomycetes with nine typifications. Fungal Systematics and Evolution 16: 1–27. https://doi.org/10.3114/fuse.2025.16.1

Li Y, He SH, Chen CC, Nakasone KK, Ma HX (2022) Global taxonomy and phylogeny of Irpicaceae (Polyporales, Basidiomycota) with descriptions of seven new species and proposals of two new combinations. Frontiers in Microbiology 13: 911978. https://doi.org/10.3389/fmicb.2022.911978

Li Y, Chen CC, He SH (2023) New corticioid taxa in Phanerochaetaceae (Polyporales, Basidiomycota) from East Asia. Frontiers in Microbiology 14: 1093096. https://doi.org/10.3389/fmicb.2023.1093096

Li Y, Cao YF, Nakasone KK, Liu SL, Huang MR, He SH (2025) Species diversity, taxonomy, multi-gene phylogeny, and divergence times of Meruliaceae (Polyporales, Basidiomycota). Mycology: 1–42. https://doi.org/10.1080/21501203.2024.2443216

Lin SH, Chen ZC (1990) The Corticiaceae and the resupinate Hydnaceae of Taiwan. Taiwania 35(2): 69–111. https://doi.org/10.1049/me:19900216

Lira CRS, Chikowski RS, de Lima VX, Gibertoni TB, Larsson KH (2022) Allophlebia, a new genus to accomodate *Phlebia ludoviciana* (Agaricomycetes, Polyporales). Mycological Progress 21(4): 1–11. https://doi.org/10.1007/s11557-022-01781-5

Liu ZB, Yuan Y (2020) *Luteoporia citriniporia* sp. nov. (Polyporales, Basidiomycota), evidenced by morphological characters and phylogenetic analysis. Phytotaxa 461: 31–39. https://doi.org/10.11646/phytotaxa.461.1.4

Liu YL, Whelen S, Hall BD (1999) Phylogenetic relationships among ascomycetes: Evidence from an RNA polymerase II subunit. Molecular Biology and Evolution 16: 1799–1808. https://doi.org/10.1093/oxfordjournals.molbev.a026092

Liu ZB, Zhang JL, Viktor P, Dai YC (2022) Taxonomy and phylogeny of Meruliaceae with descriptions of two new species from China. Journal of Fungi (Basel, Switzerland) 8(5): 501. https://doi.org/10.3390/jof8050501

Liu ZB, Liu HG, Vlasák J, Gates GM, Dai YC, Yuan Y (2025a) Global diversity and phylogeny of Incrustoporiaceae (Polyporales, Basidiomycota) with an emphasis on *Skeletocutis*. Mycology: 1–58. https://doi.org/10.1080/21501203.2024.2448145

Liu ZB, Yuan Y, Dai YC, Liu HG, Vlasák J, Zeng GY, He SH, Wu F (2025b) Global diversity and systematics of Hymenochaetaceae with non-poroid hymenophore. Fungal Diversity 131: 1–97. https://doi.org/10.1007/s13225-025-00552-3

Lutzoni F, Kauff F, Cox CJ, McLaughlin D, Celio G, Dentinger B, Padamsee M, Hibbett D, James TY, Baloch E, Grube M, Reeb V, Hofstetter V, Schoch C, Arnold AE, Miadlikowska J, Spatafora J, Johnson D, Hambleton S, Crockett M, Shoemaker R, Sung GH, Lücking R, Lumbsch T, O'Donnell K, Binder M, Diederich P, Ertz D, Gueidan C, Hansen K, Harris RC, Hosaka K, Lim YW, Matheny B, Shida H, Pfister D, Rogers J, Rossman A, Schmitt I, Sipman HJ, Stone J, Sugiyama J, Yahr R, Vilgalys RL (2004) Assembling the fungal tree of life: Progress, classification, and evolution of subcellular traits. American Journal of Botany 91: 1446–1480. https://doi.org/10.3732/ajb.91.10.1446

Ma RX, Shi ZJ, Zhao CL (2020) A new species of *Efibula* (Polyporales, Basidiomycota) from China. Phytotaxa 451(3): 238–244. https://doi.org/10.11646/phytotaxa.451.3.7

Maekawa N (1994) Taxonomic study of Japanese Corticiaceae (Aphyllophoraceae) II. Reports of the Tottori Mycological Institute 32: 1–123.

Mao WL, Wu YD, Liu HG, Yuan Y, Dai YC (2023) A contribution to *Porogramme* (Polyporaceae, Agaricomycetes) and related genera. IMA Fungus 14: 5. https://doi.org/10.1186/s43008-023-00110-z

Matheny PB (2005) Improving phylogenetic inference of mushrooms with RPB1 and RPB2 nucleotide sequences (*Inocybe*, Agaricales). Molecular Phylogenetics and Evolution 35: 1–20. https://doi.org/10.1016/j.ympev.2004.11.014

Matheny PB, Liu YJ, Ammirati JF, Hall B (2002) Using RPBI sequences to improve phylogenetic inference among mushrooms (*Inocybe*, Agaricales). American Journal of Botany 89(4): 688–698. https://doi.org/10.3732/ajb.89.4.688

Miettinen O, Larsson E, Sjökvist E, Larsson KH (2012) Comprehensive taxon sampling reveals unaccounted diversity and morphological plasticity in a group of dimitic polypores (Polyporales, Basidiomycota). Cladistics 28(3): 251–270. https://doi.org/10.1111/j.1096-0031.2011.00380.x

Miettinen O, Spirin V, Vlasak J, Rivoire B, Stenroos S, Hibbett D (2016) Polypores and genus concepts in Phanerochaetaceae (Polyporales, Basidiomycota). MycoKeys 17: 1–46. https://doi.org/10.3897/mycokeys.17.10153

Moreno G, Blanco MN, Checa J, Platas G, Peláez F (2011) Taxonomic and phylogenetic revision of three rare irpicoid species within the Meruliaceae. Mycological Progress 10(4): 481–491. https://doi.org/10.1007/s11557-010-0717-y

Motato-Vásquez V, Westphalen M, Gugliotta A (2022) *Phlebiodontia rajchenbergii* gen. et sp. nov. (Polyporales,Meruliaceae) from the Brazilian Atlantic Forest based on morphological and molecular evidence. Lilloa 59(Suplemento): 305–330. https://doi.org/10.30550/j.lil/2022.59.S/2022.09.26

Nakasone KK (2003) Type studies of resupinate hydnaceous Hymenomycetes described by Patouillard. Cryptogamie. Mycologie 24(2): 131–145.

Nakasone KK, Ortiz-Santana B, He SH (2021) Taxonomic studies of crust fungi with spines in *Radulomyces*, *Sarcodontia*, and the new genus *Noblesia*. Mycological Progress 20(11): 1479–1501. https://doi.org/10.1007/s11557-021-01746-0

Nylander JAA (2004) MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University, Uppsala, Sweden, 1–146.

Papp V, Dima B (2017) New systematic position of *Aurantiporus alborubescens* (Meruliaceae, Basidiomycota), a threatened old-growth forest polypore. Mycological Progress 17: 319–332. https://doi.org/10.1007/s11557-017-1356-3

Petersen JH (1996) Farvekort. The Danish Mycological Society´s colour-chart. Foreningen til Svampekundskabens Fremme, Greve, 1–6.

Posada D (2008) jModelTest: Phylogenetic model averaging. Molecular Biology and Evolution 25(7): 1253–1256. https://doi.org/10.1093/molbev/msn083

Qin GF, Qin WM, Wang HC, Zhao J, Korhonen K, Chen J, Dai YC, Yuan Y (2025) Phylogeny and species diversity of *Armillaria* in China based on morphological, mating test, and GCPSR criteria. Mycology 16(2): 777–811. https://doi.org/10.1080/21501203.2024.2404121

Rehner SA, Samuels GJ (1994) Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. Mycological Research 98(6): 625–634. https://doi.org/10.1016/S0953-7562(09)80409-7

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) Mrbayes 3.2: Efficient bayesian phylogenetic inference and model choice across a large model space. Molecular Systems Biology 61: 539–542. https://doi.org/10.1093/sysbio/sys029

Shen S, Ma X, Xu TM, Zhao CL (2018) *Phlebia ailaoshanensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analyses. Phytotaxa 373: 184–196. https://doi.org/10.11646/phytotaxa.373.3.2

Swofford DL (2002) PAUP*: Phylogenetic analysis using parsimony (*and Other Methods), Version 4.0b10. Sinauer Associates, Sunderland, MA, USA.

Telleria MT, Dueñas M, Martín MP (2017) Three new species of *Hydnophlebia* (Polyporales, Basidiomycota) from the Macaronesian Islands. MycoKeys 27: 39–64. https://doi.org/10.3897/mycokeys.27.14866

Tomšovský M (2012) Delimitation of an almost forgotten species *Spongipellis litschaueri* (Polyporales, Basidiomycota) and its taxonomic position within the genus. Mycological Progress 11: 415–424. https://doi.org/10.1007/s11557-011-0756-z

Tomšovský M, Menkis A, Vasaitis R (2010) Phylogenetic relationships in European *Ceriporiopsis* species inferred from nuclear and mitochondrial ribosomal DNA sequences. Fungal Biology 114: 350–358. https://doi.org/10.1016/j.funbio.2010.02.004

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172(8): 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

Vu D, Groenewald M, De Vries M, Gehrmann T, Stielow B, Eberhardt U, Verkley GJM (2019) Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology 92: 135–154. https://doi.org/10.1016/j.simyco.2018.05.001

Wang H, Zhao CL (2022) *Flavodontia rosea* gen. & sp. nov. from southwestern China. Mycotaxon 136: 755–767. https://doi.org/10.5248/136.755

Wang YR, Wu YD, Vlasák J, Yuan Y, Dai YC (2021) Phylogenetic analysis demonstrating four new species in *Megasporoporia* sensu lato (Polyporales, Basidiomycota). Mycosphere 12: 1012–1037. https://doi.org/10.5943/mycosphere/12/1/11

Wang CG, Zhao H, Liu HG, Zeng GY, Yuan Y, Dai YC (2023) A multi-gene phylogeny clarifies species diversity, taxonomy, and divergence times of *Ceriporia* and other related genera in Irpicaceae (Polyporales, Basidiomycota). Mycosphere 14(1): 1665–1729. https://doi.org/10.5943/mycosphere/14/1/19

Wang CG, Dai YC, Kout J, Gates GM, Liu HG, Yuan Y, Vlasák J (2024) Multi-gene phylogeny and taxonomy of *Physisporinus* (Polyporales, Basidiomycota). Mycosphere : Journal of Fungal Biology 15(1): 1455–1521. https://doi.org/10.5943/mycosphere/15/1/12

Wei YL, Dai YC (2004) Ecological function of wood-inhabiting fungi in forest ecosystem. Ying Yong Sheng Tai Xue Bao 15: 1935–1938.

Westphalen MC, Rajchenberg M, Tomšovský M, Gugliotta AM (2018) A re-evaluation of Neotropical *Junghuhnia* s. lat. (Polyporales, Basidiomycota) based on morphological and multigene analyses. Persoonia 41: 130. https://doi.org/10.3767/persoonia.2018.41.07

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR protocols: a guide to methods and applications, Academic Press, New York, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wu SH (1990) The Corticiaceae (Basidiomycetes) subfamilies Phlebioideae, Phanerochaetoideae and Hyphodermoideae in Taiwan. Acta Botanica Fennica 142: 1–123.

Wu F, Yuan Y, Chen JJ, He SH (2016) *Luteoporia albomarginata* gen. et sp. nov. (Meruliaceae, Basidiomycota) from tropical China. Phytotaxa 263: 31–41. https://doi.org/10.11646/phytotaxa.263.1.3

Wu F, Chen JJ, Ji XH, Vlasák J, Dai YC (2017) Phylogeny and diversity of the morphologically similar polypore genera *Rigidoporus*, *Physisporinus*, *Oxyporus*, and *Leucophellinus*. Mycologia 109: 749–765. https://doi.org/10.1080/00275514.2017.1405215

Wu F, Zhou LW, Vlasák J, Dai YC (2022a) Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. Fungal Diversity 113: 1–192. https://doi.org/10.1007/s13225-021-00496-4

Wu F, Man XW, Tohtirjap A, Dai YC (2022b) A comparison of polypore funga and species composition in forest ecosystems of China, North America, and Europe. Forest Ecosystems 9: 100051. https://doi.org/10.1016/j.fecs.2022.100051

Xu TM, Sun YF, Liu S, Song CG, Gao N, Wu DM, Cui BK (2023) *Ceriporiopsis tianshanensis* (Polyporales, Agaricomycetes) and *Sidera tianshanensis* (Hymenochaetales, Agaricomycetes), two new species of wood-inhabiting fungi from Xinjiang, Northwest China. MycoKeys 98: 1–18. https://doi.org/10.3897/mycokeys.98.102552

Xu TM, Wu DM, Gao N, Liu S, Sun YF, Cui BK (2024) Species diversity, taxonomic classification and ecological habits of polypore fungi in China. Mycology 16(2): 419–544. https://doi.org/10.1080/21501203.2024.2384567

Yang Y, Li R, Liu CM, Zhao CL (2023) Morphological and molecular identification for two new species of wood-inhabiting macrofungi (Basidiomycota) from Yunnan-Guizhou Plateau, China. Phytotaxa 591: 1–18. https://doi.org/10.11646/phytotaxa.591.1.1

Yang Y, Li R, Jiang QQ, Zhou HM, Muhammad A, Wang HJ, Zhao CL (2024) Phylogenetic and taxonomic analyses reveal three new wood-inhabiting fungi (Polyporales, Basidiomycota) in China. Journal of Fungi (Basel, Switzerland) 10(1): 55. https://doi.org/10.3390/jof10010055

Yang Y, Xu Y, Wang L, Jiang QQ, Su JQ, Li R, Zhou HM, Zhao CL (2025a) Multigene phylogeny of seven wood-inhabiting fungal orders in Basidiomycota, and proposal of a new genus and thirteen new species. Mycosphere 16(1): 245–295. https://doi.org/10.5943/mycosphere/16/1/4

Yang X, Zhu YG, Duan SJ, Wu XX, Zhao CL (2025b) Morphology and multigene phylogeny revealed four new species of *Geastrum* (Geastrales, Basidiomycota) from China. MycoKeys 113: 73–100. https://doi.org/10.3897/mycokeys.113.139672

Yuan Y, Bian LS, Wu YD, Chen JJ, Wu F, Liu HG, Zeng GY, Dai YC (2023) Species diversity of pathogenic wood-rotting fungi (Agaricomycetes, Basidiomycota) in China. Mycology 14: 204–226. https://doi.org/10.1080/21501203.2023.2238779

Zhang QY, Liu HG, Papp V, Zhou M, Dai YC, Yuan Y (2023) New insights into the classification and evolution of *Favolaschia* (Agaricales, Basidiomycota) and its poten-

tial distribution, with descriptions of eight new species. Mycosphere 14: 777–814. https://doi.org/10.5943/mycosphere/14/1/10

Zhang X, Zhou HM, Ghobad-Nejhad M, Liu HG (2024) Molecular and morphological data reveal two new polypores (Polyporales, Basidiomycota) with reddish brown to orange basidiomata from China. MycoKeys 107: 75–94. https://doi.org/10.3897/mycokeys.107.126176

Zhang JL, Gu ZR, Zhou CQ, Zhou HM (2025) Molecular phylogeny and morphology reveal four new species in Hymenochaetales and one new species in Cantharellales from Southwestern China. MycoKeys 115: 87–135. https://doi.org/10.3897/mycokeys.115.142433

Zhao CL, Cui BK (2014) Phylogeny and taxonomy of *Ceriporiopsis* (Polyporales) with descriptions of two new species from southern China. Phytotaxa 164: 17–28. https://doi.org/10.11646/phytotaxa.164.1.2

Zhao CL, Wu ZQ (2017) *Ceriporiopsis kunmingensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. Mycological Progress 16: 93–100. https://doi.org/10.1007/s11557-016-1259-8

Zhao CL, Cui BK, Dai YC (2012) New species and phylogeny of *Perenniporia* based on morphological and molecular characters. Fungal Diversity 58: 47–60. https://doi.org/10.1007/s13225-012-0177-6

Zhao CL, Ren GJ, Wu F (2017) A new species of *Hyphodermella* (Polyporales, Basidiomycota) with a poroid hymenophore. Mycoscience 58: 452–456. https://doi.org/10.1016/j.myc.2017.06.007

Zhao CL, Qu MH, Huang RX, Karunarathna SC (2023) Multi-gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (Polyporales, Basidiomycota). Journal of Fungi (Basel, Switzerland) 9: 320. https://doi.org/10.3390/jof9030320

Zhao H, Wu YD, Yang ZR, Liu HG, Wu F, Dai YC, Yuan Y (2024) Polypore funga and species diversity in tropical forest ecosystems of Africa, America and Asia, and a comparison with temperate and boreal regions of the Northern Hemisphere. Forest Ecosystems 11: 100200. https://doi.org/10.1016/j.fecs.2024.100200

Zhou HM, Yang X, Wang YY, Zhao CL (2024) Morphological and molecular identification of two new wood-inhabiting macrofungi (Basidiomycota) from Yunnan-Guizhou Plateau, China. Phytotaxa 674(1): 1–17. https://doi.org/10.11646/phytotaxa.674.1.1

Zhou HM, Dai YC, Bian LS, Liu HG, Vlasák J, Yuan Y (2025) Diversity, divergence time, and biogeography of the genus *Albatrellus* (Agaricomycetes, Russulales). Mycology 16(2): 738–776. https://doi.org/10.1080/21501203.2024.2386021

Zmitrovich IV (2018) Conspectus systematis Polyporacearum v. 1.0. Folia Cryptogamica Petropolitana 6: 3–145.

Zmitrovich IV, Malysheva VF (2014) Studies on *Oxyporus*. I. Segregation of *Emmia* and general topology of phylogenetic tree. Mycology Phytopathology 48: 161–171.

Zong TK, Zhao CL (2021) Morphological and molecular identification of two new species of *Phlebiella* (Polyporales, Basidiomycota) from southern China. Nova Hedwigia 112(3-4): 501–514. https://doi.org/10.1127/nova_hedwigia/2021/0628